

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Lin, Lih-Ling
Chen, Jennifer H.
Schievella, Andrea
Graham, James
- (ii) TITLE OF INVENTION: NOVEL TNF RECEPTOR DEATH DOMAIN LIGAND
PROTEINS AND INHIBITORS OF LIGAND BINDING
- (iii) NUMBER OF SEQUENCES: 18
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Genetics Institute, Inc.
 - (B) STREET: 87 CambridgePark Drive
 - (C) CITY: Cambridge
 - (D) STATE: Massachusetts
 - (E) COUNTRY: USA
 - (F) ZIP: 02140
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE:
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Brown, Scott A,
 - (B) REGISTRATION NUMBER: 32,724
 - (C) REFERENCE/DOCKET NUMBER: GI5232D
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (617) 498-8224
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(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2158 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 2..1231

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

C AGC AAT GCA GGT GAT GGA CCA GGT GGC GAG GGC AGT GTT CAC CTG
 Ser Asn Ala Gly Asp Gly Pro Gly Gly Glu Gly Ser Val His Leu
 1 5 10 15

46

GCA Ala	AGC Ser	TCT Ser	CGG Arg	GGC Gly 20	ACT Thr	TTG Leu	TCT Ser	GAT Asp	AGT Ser 25	GAA Glu	ATT Ile	GAG Glu	ACC Thr	AAC Asn 30	TCT Ser	94
GCC Ala	ACA Thr	AGC Ser	ACC Thr 35	ATC Ile	TTT Phe	GGT Gly	AAA Lys 40	GCC Ala	CAC His	AGC Ser	TTG Leu	AAG Lys	CCA Pro 45	AGC Ser	ATA Ile	142
AAG Lys	GAG Glu	AAG Lys 50	CTG Leu	GCA Ala	GGC Gly	AGC Ser	CCC Pro 55	ATT Ile	CGT Arg	ACT Thr	TCT Ser	GAA Glu 60	GAT Asp	GTG Val	AGC Ser	190
CAG Gln	CGA Arg 65	GTC Val	TAT Tyr	CTC Leu	TAT Tyr 70	GAG Glu 70	GGA Gly	CTC Leu	CTA Leu	GGC Gly	AAA Lys 75	GAG Glu	CGT Arg	TCT Ser	ACT Thr	238
TTA Leu 80	TGG Trp	GAC Asp	CAA Gln	ATG Met	CAA Gln 85	TTC Phe	TGG Trp	GAA Glu	GAT Asp	GCC Ala 90	TTC Phe	TTA Leu	GAT Asp	GCT Ala	GTG Val 95	286
ATG Met	TTG Leu	GAG Glu	AGA Arg	GAA Glu 100	GGG Gly	ATG Met	GGT Gly	ATG Met	GAC Asp 105	CAG Gln	GGT Gly	CCC Pro	CAG Gln	GAA Glu 110	ATG Met	334
ATC Ile	GAC Asp	AGG Arg	TAC Tyr 115	CTG Leu	TCC Ser	CTT Leu	GGA Gly	GAA Glu 120	CAT His	GAC Asp	CGG Arg	AAG Lys	CGC Arg 125	CTG Leu	GAA Glu	382
GAT Asp	GAT Asp	GAA Glu 130	GAT Asp	CGC Arg	TTG Leu	CTG Leu	GCC Ala 135	ACA Thr	CTT Leu	CTG Leu	CAC His	AAC Asn 140	CTC Leu	ATC Ile	TCC Ser	430
TAC Tyr	ATG Met 145	CTG Leu	CTG Leu	ATG Met	AAG Lys	GTA Val 150	AAT Asn	AAG Lys	AAT Asn	GAC Asp	ATC Ile 155	CGC Arg	AAG Lys	AAG Lys	GTG Val	478
AGG Arg 160	CGC Arg	CTA Leu	ATG Met	GGA Gly 165	AAG Lys 165	TCG Ser	CAC His	ATT Ile	GGG Gly 170	CTT Leu	GTG Val	TAC Tyr	AGC Ser	CAG Gln 175	CAA Gln 175	526
ATC Ile	AAT Asn	GAG Glu	GTG Val 180	CTT Leu	GAT Asp	CAG Gln	CTG Leu	GCG Ala	AAC Asn 185	CTG Leu	AAT Asn	GGA Gly	CGC Arg	GAT Asp 190	CTC Leu	574
TCT Ser	ATC Ile	TGG Trp	TCC Ser 195	AGT Ser	GGC Gly	AGC Ser	CGG Arg	CAC His 200	ATG Met	AAG Lys	AAG Lys	CAG Gln	ACA Thr 205	TTT Phe	GTG Val	622
GTA Val	CAT His	GCA Ala 210	GGG Gly	ACA Thr	GAT Asp	ACA Thr	AAC Asn 215	GGA Gly	GAT Asp	ATC Ile	TTT Phe	TTC Phe	ATG Met	GAG Glu	GTG Val	670
TGC Cys	GAT Asp 225	GAC Asp	TGT Cys	GTG Val	GTG Val	TTG Leu 230	CGT Arg	AGT Ser	AAC Asn	ATC Ile	GGA Gly 235	ACA Thr	GTG Val	TAT Tyr	GAG Glu	718
CGC Arg 240	TGG Trp	TGG Trp	TAC Tyr	GAG Glu	AAG Lys 245	CTC Leu	ATC Ile	AAC Asn	ATG Met	ACC Thr 250	TAC Tyr	TGT Cys	CCC Pro	AAG Lys	ACG Thr 255	766
AAG Lys	GTG Val	TTG Leu	TGC Cys 260	TTG Leu 260	TGG Trp	CGT Arg	AGA Arg	AAT Asn	GGC Gly 265	TCT Ser	GAG Glu	ACC Thr	CAG Gln 270	CTC Leu 270	AAC Asn	814

[illegible]

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 410 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

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Ser Asn Ala Gly Asp Gly Pro Gly Gly Glu Gly Ser Val His Leu Ala
 1           5           10
Ser Ser Arg Gly Thr Leu Ser Asp Ser Glu Ile Glu Thr Asn Ser Ala
          20           25           30
Thr Ser Thr Ile Phe Gly Lys Ala His Ser Leu Lys Pro Ser Ile Lys
          35           40           45
Glu Lys Leu Ala Gly Ser Pro Ile Arg Thr Ser Glu Asp Val Ser Gln
          50           55           60
Arg Val Tyr Leu Tyr Glu Gly Leu Leu Gly Lys Glu Arg Ser Thr Leu
          65           70           75           80
Trp Asp Gln Met Gln Phe Trp Glu Asp Ala Phe Leu Asp Ala Val Met
          85           90           95
Leu Glu Arg Glu Gly Met Gly Met Asp Gln Gly Pro Gln Glu Met Ile
          100          105          110
Asp Arg Tyr Leu Ser Leu Gly Glu His Asp Arg Lys Arg Leu Glu Asp
          115          120          125
Asp Glu Asp Arg Leu Leu Ala Thr Leu Leu His Asn Leu Ile Ser Tyr
          130          135          140
Met Leu Leu Met Lys Val Asn Lys Asn Asp Ile Arg Lys Lys Val Arg
          145          150          155          160
Arg Leu Met Gly Lys Ser His Ile Gly Leu Val Tyr Ser Gln Gln Ile
          165          170          175
Asn Glu Val Leu Asp Gln Leu Ala Asn Leu Asn Gly Arg Asp Leu Ser
          180          185          190
Ile Trp Ser Ser Gly Ser Arg His Met Lys Lys Gln Thr Phe Val Val
          195          200          205
His Ala Gly Thr Asp Thr Asn Gly Asp Ile Phe Phe Met Glu Val Cys
          210          215          220
Asp Asp Cys Val Val Leu Arg Ser Asn Ile Gly Thr Val Tyr Glu Arg
          225          230          235          240
Trp Trp Tyr Glu Lys Leu Ile Asn Met Thr Tyr Cys Pro Lys Thr Lys
          245          250          255
Val Leu Cys Leu Trp Arg Arg Asn Gly Ser Glu Thr Gln Leu Asn Lys
          260          265          270
Phe Tyr Thr Lys Lys Cys Arg Glu Leu Tyr Tyr Cys Val Lys Asp Ser
          275          280          285

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09989350 142004

Met Glu Arg Ala Ala Ala Arg Gln Gln Ser Ile Lys Pro Gly Pro Glu
290 295 300
Leu Gly Gly Glu Phe Pro Val Gln Asp Leu Lys Thr Gly Glu Gly Gly
305 310 315 320
Leu Leu Gln Val Thr Leu Glu Gly Ile Asn Leu Lys Phe Met His Asn
325 330 335
Gln Val Phe Ile Glu Leu Asn His Ile Lys Lys Cys Asn Thr Val Arg
340 345 350
Gly Val Phe Val Leu Glu Glu Phe Val Pro Glu Ile Lys Glu Val Val
355 360 365
Ser His Lys Tyr Lys Thr Pro Met Ala His Glu Ile Cys Tyr Ser Val
370 375 380
Leu Cys Leu Phe Ser Tyr Val Ala Ala Val His Ser Ser Glu Glu Asp
385 390 395 400
Leu Arg Thr Pro Pro Arg Pro Val Ser Ser
405 410

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 826 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 2..415

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

G GAG GTG CAG GAC CTC TTC GAA GCC CAG GGC AAT GAC CGA CTG AAG	46
Glu Val Gln Asp Leu Phe Glu Ala Gln Gly Asn Asp Arg Leu Lys	
1 5 10 15	
CTG CTG GTG CTG TAC AGT GGA GAG GAT GAT GAG CTG CTA CAG CGG GCA	94
Leu Leu Val Leu Tyr Ser Gly Glu Asp Asp Glu Leu Leu Gln Arg Ala	
20 25 30	
GCT GCC GGG GGC TTG GCC ATG CTT ACC TCC ATG CGG CCC ACG CTC TGC	142
Ala Ala Gly Gly Leu Ala Met Leu Thr Ser Met Arg Pro Thr Leu Cys	
35 40 45	
AGC CGC ATT CCC CAA GTG ACC ACA CAC TGG CTG GAG ATC CTG CAG GCC	190
Ser Arg Ile Pro Gln Val Thr His Trp Leu Glu Ile Leu Gln Ala	
50 55 60	
CTG CTT CTG AGC TCC AAC CAG GAG CTG CAG CAC CGG GGT GCT GTG GTG	238
Leu Leu Ser Ser Asn Gln Glu Leu Gln His Arg Gly Ala Val Val	
65 70 75	
GTG CTG AAC ATG GTG GAG GCC TCG AGG GAG ATT GCC AGC ACC CTG ATG	286
Val Leu Asn Met Val Glu Ala Ser Arg Glu Ile Ala Ser Thr Leu Met	
80 85 90 95	

GAG AGT GAG ATG ATG GAG ATC TTG TCA GTG CTA GCT AAG GGT GAC CAC	334
Glu Ser Glu Met Met Glu Ile Leu Ser Val Leu Ala Lys Gly Asp His	
100 105 110	
AGC CCT GTC ACA AGG GCT GCT GCA GCC TGC CTG GAC AAA GCA GTG GAA	382
Ser Pro Val Thr Arg Ala Ala Ala Ala Cys Leu Asp Lys Ala Val Glu	
115 120 125	
TAT GGG CTT ATC CAA CCC AAC CAA GAT GGA GAG TGAGGGGGTT GTCCCTGGGC	435
Tyr Gly Leu Ile Gln Pro Asn Gln Asp Gly Glu	
130 135	
CCAAGGCTCA TGCACACGCT ACCTATTGTG GCACGGAGAG TAAGGACGGA AGCAGCTTTG	495
GCTGGTGGTG GCTGGCATGC CCAATACTCT TGCCCATCCT CGCTTGCTGC CCTAGGATGT	555
CCTCTGTTCT GAGTCAGCGG CCACGTTTCTG TCACACAGCC CTGCTTGGCC AGCACTGCCT	615
GCAGCCTCAC TCAGAGGGGC CCTTTTCTG TACTACTGTA GTCAGCTGGG AATGGGGAAG	675
GTGCATCCCA ACACAGCCTG TGGATCCTGG GGCATTTGGA AGGGCGCACA CATCAGCAGC	735
CTCACCAGCT GTGAGCCTGC TATCAGGCCT GCCCCTCCAA TAAAAGTGTG TAGAACTCCA	795
AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA A	826

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 138 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Glu Val Gln Asp Leu Phe Glu Ala Gln Gly Asn Asp Arg Leu Lys Leu	
1 5 10 15	
Leu Val Leu Tyr Ser Gly Glu Asp Asp Glu Leu Leu Gln Arg Ala Ala	
20 25 30	
Ala Gly Gly Leu Ala Met Leu Thr Ser Met Arg Pro Thr Leu Cys Ser	
35 40 45	
Arg Ile Pro Gln Val Thr Thr His Trp Leu Glu Ile Leu Gln Ala Leu	
50 55 60	
Leu Leu Ser Ser Asn Gln Glu Leu Gln His Arg Gly Ala Val Val Val	
65 70 75 80	
Leu Asn Met Val Glu Ala Ser Arg Glu Ile Ala Ser Thr Leu Met Glu	
85 90 95	
Ser Glu Met Met Glu Ile Leu Ser Val Leu Ala Lys Gly Asp His Ser	
100 105 110	
Pro Val Thr Arg Ala Ala Ala Ala Cys Leu Asp Lys Ala Val Glu Tyr	
115 120 125	
Gly Leu Ile Gln Pro Asn Gln Asp Gly Glu	
130 135	

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 722 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

- (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 2..559

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

G GAG AAG CCG CTG CAC GCC CTG CTG CAC GGC CGC GGG GTT TGC CTC	46
Glu Lys Pro Leu His Ala Leu Leu His Gly Arg Gly Val Cys Leu	
1 5 10 15	
AAC GAA AAG AGC TAC CGC GAG CAA GTC AAG ATC GAG AGA GAC TCC CGT	94
Asn Glu Lys Ser Tyr Arg Glu Gln Val Lys Ile Glu Arg Asp Ser Arg	
20 25 30	
GAG CAC GAG GAG CCC ACC ACC TCT GAG ATG GCC GAG GAG ACC TAC TCC	142
Glu His Glu Glu Pro Thr Thr Ser Glu Met Ala Glu Glu Thr Tyr Ser	
35 40 45	
CCC AAG ATC TTC CGG CCC AAA CAC ACC CGC ATC TCC GAG CTG AAG GCT	190
Pro Lys Ile Phe Arg Pro Lys His Thr Arg Ile Ser Glu Leu Lys Ala	
50 55 60	
GAA GCA GTG AAG AAG GAC CGC AGA AAG AAG CTG ACC CAG TCC AAG TTT	238
Glu Ala Val Lys Lys Asp Arg Arg Lys Lys Leu Thr Gln Ser Lys Phe	
65 70 75	
GTC GGG GGA GCC GAG AAC ACT GCC CAC CCC CGG ATC ATC TCT GAA CCT	286
Val Gly Gly Ala Glu Asn Thr Ala His Pro Arg Ile Ile Ser Glu Pro	
80 85 90 95	
GAG ATG AGA CAG GAG TCT GAG CAG GGC CCC TGC CGC AGA CAC ATG GAG	334
Glu Met Arg Gln Glu Ser Glu Gln Gly Pro Cys Arg Arg His Met Glu	
100 105 110	
GCT TCC CTG CAG GAG CTC AAA GCC AGC CCA CGC ATG GTG CCC CGT GCT	382
Ala Ser Leu Gln Glu Leu Lys Ala Ser Pro Arg Met Val Pro Arg Ala	
115 120 125	
GTG TAC CTG CCC AAT TGT GAC CGC AAA GGA TTC TAC AAG AGA AAG CAG	430
Val Tyr Leu Pro Asn Cys Asp Arg Lys Gly Phe Tyr Lys Arg Lys Gln	
130 135 140	
TGC AAA CCT TCC CGT GGC CGC AAG CGT GGC ATC TGC TGG TGC GTG GAC	478
Cys Lys Pro Ser Arg Gly Arg Lys Arg Gly Ile Cys Trp Cys Val Asp	
145 150 155	
AAG TAC GGG ATG AAG CTG CCA GGC ATG GAG TAC GTT GAC GGG GAC TTT	526
Lys Tyr Gly Met Lys Leu Pro Gly Met Glu Tyr Val Asp Gly Asp Phe	
160 165 170 175	
CAG TGC CAC ACC TTC GAC AGC AGC AAC GTT GAG TGATGCGTCC CCCCCAACCC	579
Gln Cys His Thr Phe Asp Ser Ser Asn Val Glu	
180 185	
TTTCCCTCAC CCCCTTCCAC CCCCAGCCCC GACTCCAGCC AGCGCCTCCC TCCACCCCAG	639

GACGCCACTC ATTTTCATCTC ATTTAAGGGA AAAATATATA TCTATCTATT TGAGGAAAAA 699
 AAAAAAAAAA AAAAAAAAAA AAA 722

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 186 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Glu Lys Pro Leu His Ala Leu Leu His Gly Arg Gly Val Cys Leu Asn
 1 5 10 15
 Glu Lys Ser Tyr Arg Glu Gln Val Lys Ile Glu Arg Asp Ser Arg Glu
 20 25 30
 His Glu Glu Pro Thr Thr Ser Glu Met Ala Glu Glu Thr Tyr Ser Pro
 35 40 45
 Lys Ile Phe Arg Pro Lys His Thr Arg Ile Ser Glu Leu Lys Ala Glu
 50 55 60
 Ala Val Lys Lys Asp Arg Arg Lys Lys Leu Thr Gln Ser Lys Phe Val
 65 70 75 80
 Gly Gly Ala Glu Asn Thr Ala His Pro Arg Ile Ile Ser Glu Pro Glu
 85 90 95
 Met Arg Gln Glu Ser Glu Gln Gly Pro Cys Arg Arg His Met Glu Ala
 100 105 110
 Ser Leu Gln Glu Leu Lys Ala Ser Pro Arg Met Val Pro Arg Ala Val
 115 120 125
 Tyr Leu Pro Asn Cys Asp Arg Lys Gly Phe Tyr Lys Arg Lys Gln Cys
 130 135 140
 Lys Pro Ser Arg Gly Arg Lys Arg Gly Ile Cys Trp Cys Val Asp Lys
 145 150 155 160
 Tyr Gly Met Lys Leu Pro Gly Met Glu Tyr Val Asp Gly Asp Phe Gln
 165 170 175
 Cys His Thr Phe Asp Ser Ser Asn Val Glu
 180 185

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1023 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

- (ix) FEATURE:
 (A) NAME/KEY: CDS

[illegible][illegible][illegible]

TGC TGG TGC GTG GAC AAG TAC GGG ATG AAG CTG CCA GGC ATG GAG TAC	824
Cys Trp Cys Val Asp Lys Tyr Gly Met Lys Leu Pro Gly Met Glu Tyr	
245 250 255	
GTT GAC GGG GAC TTT CAG TGC CAC ACC TTC GAC AGC AGC AAC GTT GAG	872
Val Asp Gly Asp Phe Gln Cys His Thr Phe Asp Ser Ser Asn Val Glu	
260 265 270	
TGATGCGTCC CCCCCCAACC TTCCCTCAC CCCCTCCCAC CCCCAGCCCC GACTCCAGCC	932
AGCGCCTCCC TCCACCCAG GACGCCACTC ATTCATCTC ATTTAAGGGA AAAATATATA	992
TCTATCTATT TGAAAAAAAA AAAAAAACC C	1023

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 272 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Val Leu Leu Thr Ala Val Leu Leu Leu Leu Ala Ala Tyr Ala Gly	
1 5 10 15	
Pro Ala Gln Ser Leu Gly Ser Phe Val His Cys Glu Pro Cys Asp Glu	
20 25 30	
Lys Ala Leu Ser Met Cys Pro Pro Ser Pro Leu Gly Cys Glu Leu Val	
35 40 45	
Lys Glu Pro Gly Cys Gly Cys Cys Met Thr Cys Ala Leu Ala Glu Gly	
50 55 60	
Gln Ser Cys Gly Val Tyr Thr Glu Arg Cys Ala Gln Gly Leu Arg Cys	
65 70 75 80	
Leu Pro Arg Gln Asp Glu Glu Lys Pro Leu His Ala Leu Leu His Gly	
85 90 95	
Arg Gly Val Cys Leu Asn Glu Lys Ser Tyr Arg Glu Gln Val Lys Ile	
100 105 110	
Glu Arg Asp Ser Arg Glu His Glu Glu Pro Thr Thr Ser Glu Met Ala	
115 120 125	
Glu Glu Thr Tyr Ser Pro Lys Ile Phe Arg Pro Lys His Thr Arg Ile	
130 135 140	
Ser Glu Leu Lys Ala Glu Ala Val Lys Lys Asp Arg Arg Lys Lys Leu	
145 150 155 160	
Thr Gln Ser Lys Phe Val Gly Gly Ala Glu Asn Thr Ala His Pro Arg	
165 170 175	
Ile Ile Ser Ala Pro Glu Met Arg Gln Glu Ser Glu Gln Gly Pro Cys	
180 185 190	
Arg Arg His Met Glu Ala Ser Leu Gln Glu Leu Lys Ala Ser Pro Arg	
195 200 205	
Met Val Pro Arg Ala Val Tyr Leu Pro Asn Cys Asp Arg Lys Gly Phe	
210 215 220	

Tyr Lys Arg Lys Gln Cys Lys Pro Ser Arg Gly Arg Lys Arg Gly Ile
 225 230 235 240
 Cys Trp Cys Val Asp Lys Tyr Gly Met Lys Leu Pro Gly Met Glu Tyr
 245 250 255
 Val Asp Gly Asp Phe Gln Cys His Thr Phe Asp Ser Ser Asn Val Glu
 260 265 270

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1694 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

- (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 2..931

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

C TCT CTC AAG GCC AAC ATC CCT GAG GTG GAA GCT GTC CTC AAC ACC	46
Ser Leu Lys Ala Asn Ile Pro Glu Val Glu Ala Val Leu Asn Thr	
1 5 10 15	
GAC AGG AGT TTG GTG TGT GAT GGG AAG AGG GGC TTA TTA ACT CGT CTG	94
Asp Arg Ser Leu Val Cys Asp Gly Lys Arg Gly Leu Leu Thr Arg Leu	
20 25 30	
CTG CAG GTC ATG AAG AAG GAG CCA GCA GAG TCG TCT TTC AGG TTT TGG	142
Leu Gln Val Met Lys Lys Glu Pro Ala Glu Ser Ser Phe Arg Phe Trp	
35 40 45	
CAA GCT CGG GCT GTG GAG AGT TTC CTC CGA GGG ACC ACC TCC TAT GCA	190
Gln Ala Arg Ala Val Glu Ser Phe Leu Arg Gly Thr Thr Ser Tyr Ala	
50 55 60	
GAC CAG ATG TTC CTG CTG AAG CGA GGC CTC TTG GAG CAC ATC CTT TAC	238
Asp Gln Met Phe Leu Leu Lys Arg Gly Leu Leu Glu His Ile Leu Tyr	
65 70 75	
TGC ATT GTG GAC AGC GAG TGT AAG TCA AGG GAT GTG CTC CAG AGT TAC	286
Cys Ile Val Asp Ser Glu Cys Lys Ser Arg Asp Val Leu Gln Ser Tyr	
80 85 90 95	
TTT GAC CTC CTG GGG GAG CTG ATG AAG TTC AAC GTT GAT GCA TTC AAG	334
Phe Asp Leu Leu Gly Glu Leu Met Lys Phe Asn Val Asp Ala Phe Lys	
100 105 110	
AGA TTC AAT AAA TAT ATC AAC ACC GAT GCA AAG TTC CAG GTA TTC CTG	382
Arg Phe Asn Lys Tyr Ile Asn Thr Asp Ala Lys Phe Gln Val Phe Leu	
115 120 125	

09989350 112001

AAG CAG ATC AAC AGC TCC CTG GTG GAC TCC AAC ATG CTG GTG CGC TGT Lys Gln Ile Asn Ser Ser Leu Val Asp Ser Asn Met Leu Val Arg Cys 130 135 140	430
GTC ACT CTG TCC CTG GAC CGA TTT GAA AAC CAG GTG GAT ATG AAA GTT Val Thr Leu Ser Leu Asp Arg Phe Glu Asn Gln Val Asp Met Lys Val 145 150 155	478
GCC GAG GTA CTG TCT GAA TGC CGC CTG CTC GCC TAC ATA TCC CAG GTG Ala Glu Val Leu Ser Glu Cys Arg Leu Leu Ala Tyr Ile Ser Gln Val 160 165 170 175	526
CCC ACG CAG ATG TCC TTC CTC TTC CGC CTC ATC AAC ATC ATC CAC GTG Pro Thr Gln Met Ser Phe Leu Phe Arg Leu Ile Asn Ile Ile His Val 180 185 190	574
CAG ACG CTG ACC CAG GAG AAC GTC AGC TGC CTC AAC ACC AGC CTG GTG Gln Thr Leu Thr Gln Glu Asn Val Ser Cys Leu Asn Thr Ser Leu Val 195 200 205	622
ATC CTG ATG CTG GCC CGA CGG AAA GAG CGG CTG CCC CTG TAC CTG CGG Ile Leu Met Leu Ala Arg Arg Lys Glu Arg Leu Pro Leu Tyr Leu Arg 210 215 220	670
CTG CTG CAG CGG ATG GAG CAC AGC AAG AAG TAC CCC GGC TTC CTG CTC Leu Leu Gln Arg Met Glu His Ser Lys Lys Tyr Pro Gly Phe Leu Leu 225 230 235	718
AAC AAC TTC CAC AAC CTG CTG CGC TTC TGG CAG CAG CAC TAC CTG CAC Asn Asn Phe His Asn Leu Leu Arg Phe Trp Gln Gln His Tyr Leu His 240 245 250 255	766
AAG GAC AAG GAC AGC ACC TGC CTA GAG AAC AGC TCC TGC ATC AGC TTC Lys Asp Lys Asp Ser Thr Cys Leu Glu Asn Ser Ser Cys Ile Ser Phe 260 265 270	814
TCA TAC TGG AAG GAG ACA GTG TCC ATC CTG TTG AAC CCG GAC CGG CAG Ser Tyr Trp Lys Glu Thr Val Ser Ile Leu Leu Asn Pro Asp Arg Gln 275 280 285	862
TCA CCC TCT GCT CTC GTT AGC TAC ATT GAG GAG CCC TAC ATG GAC ATA Ser Pro Ser Ala Leu Val Ser Tyr Ile Glu Glu Pro Tyr Met Asp Ile 290 295 300	910
GAC AGG GAC TTC ACT GAG GAG TGACCTTGGG CCAGGCCTCG GGAGGCTGCT Asp Arg Asp Phe Thr Glu Glu 305 310	961
GGGCCAGTGT GGGTGAGCGT GGGTACGATG CCACACGCCC TGCCCTGTTC CCGTTCCTCC	1021
CTGCTGCTCT CTGCCTGCCC CAGGTCTTTG GGTACAGGCT TGGTGGGAGG GAAGTCCTAG	1081
AAGCCCTTGG TCCCCCTGGG TCTGAGGGCC CTAGGTCATG GAGAGCCTCA GTCCCCATAA	1141
TGAGGACAGG GTACCATGCC CACCTTTCCT TCAGAACCCT GGGGCCCAGG GCCACCCAGA	1201
GGTAAGAGGA CATTTAGCAT TAGCTCTGTG TGAGCTCCTG CCGGTTTCTT GGCTGTCACT	1261
CAGTCCCAGA GTGGGGAGGA AGATATGGGT GACCCCCACC CCCCATCTGT GAGCCAAGCC	1321
TCCCTTGTC CTGGCCTTTG GACCCAGGCA AAGGCTTCTG AGCCCTGGGC AGGGGTGGTG	1381
GGTACCAGAG AATGCTGCCT TCCCCAAGC CTGCCCTCT GCCTCATTTT CCTGTAGCTC	1441
CTCTGGTTCT GTTTGCTCAT TGGCCGCTGT GTTCATCCAA GGGGGTTCTC CCAGAAAGTA	1501
GGGGCCTTTC CCTCCATCCC TTGGGGCAG GGGCAGCTGT GCCTGCCCTG CCTCTGCCTG	1561

AGGCAGCCGC TCCTGCCTGA GCCTGGACAT GGGGCCCTTC CTTGTGTTGC CAATTTATTA 1621
 ACAGCAAATA AACCAATTAA ATGGAGACTA TTAAATAACT TTATTTTAAA AATGAAAAAA 1681
 AAAAAAAAAA AAA 1694

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 310 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Ser Leu Lys Ala Asn Ile Pro Glu Val Glu Ala Val Leu Asn Thr Asp
 1 5 10 15
 Arg Ser Leu Val Cys Asp Gly Lys Arg Gly Leu Leu Thr Arg Leu Leu
 20 25 30
 Gln Val Met Lys Lys Glu Pro Ala Glu Ser Ser Phe Arg Phe Trp Gln
 35 40 45
 Ala Arg Ala Val Glu Ser Phe Leu Arg Gly Thr Thr Ser Tyr Ala Asp
 50 55 60
 Gln Met Phe Leu Leu Lys Arg Gly Leu Leu Glu His Ile Leu Tyr Cys
 65 70 75 80
 Ile Val Asp Ser Glu Cys Lys Ser Arg Asp Val Leu Gln Ser Tyr Phe
 85 90 95
 Asp Leu Leu Gly Glu Leu Met Lys Phe Asn Val Asp Ala Phe Lys Arg
 100 105 110
 Phe Asn Lys Tyr Ile Asn Thr Asp Ala Lys Phe Gln Val Phe Leu Lys
 115 120 125
 Gln Ile Asn Ser Ser Leu Val Asp Ser Asn Met Leu Val Arg Cys Val
 130 135 140
 Thr Leu Ser Leu Asp Arg Phe Glu Asn Gln Val Asp Met Lys Val Ala
 145 150 155 160
 Glu Val Leu Ser Glu Cys Arg Leu Leu Ala Tyr Ile Ser Gln Val Pro
 165 170 175
 Thr Gln Met Ser Phe Leu Phe Arg Leu Ile Asn Ile Ile His Val Gln
 180 185 190
 Thr Leu Thr Gln Glu Asn Val Ser Cys Leu Asn Thr Ser Leu Val Ile
 195 200 205
 Leu Met Leu Ala Arg Arg Lys Glu Arg Leu Pro Leu Tyr Leu Arg Leu
 210 215 220
 Leu Gln Arg Met Glu His Ser Lys Lys Tyr Pro Gly Phe Leu Leu Asn
 225 230 235 240
 Asn Phe His Asn Leu Leu Arg Phe Trp Gln Gln His Tyr Leu His Lys
 245 250 255
 Asp Lys Asp Ser Thr Cys Leu Glu Asn Ser Ser Cys Ile Ser Phe Ser

[illegible]

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2735 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(iii) HYPOTHETICAL: NO

(A) NAME/KEY: CDS
(B) LOCATION: 2..1822

G	GAG	ATC	AGT	CGG	AAG	GTG	TAC	AAG	GGA	ATG	TTA	GAC	CTC	CTC	AAG	46
Glu	Ile	Ser	Arg	Lys	Val	Tyr	Lys	Gly	Met	Leu	Asp	Leu	Leu	Lys		
1				5				10					15			
TGT	ACA	GTC	CTC	AGC	TTG	GAG	CAG	TCC	TAT	GCC	CAC	GCG	GGT	CTG	GGT	94
Cys	Thr	Val	Leu	Ser	Leu	Glu	Gln	Ser	Tyr	Ala	His	Ala	Gly	Leu	Gly	
				20				25						30		
GGC	ATG	GCC	AGC	ATC	TTT	GGG	CTT	TTG	GAG	ATT	GCC	CAG	ACC	CAC	TAC	142
Gly	Met	Ala	Ser	Ile	Phe	Gly	Leu	Leu	Glu	Ile	Ala	Gln	Thr	His	Tyr	
			35					40				45				
TAT	AGT	AAA	GAA	CCA	GAC	AAG	CGG	AAG	AGA	AGT	CCA	ACA	GAA	AGT	GTA	190
Tyr	Ser	Lys	Glu	Pro	Asp	Lys	Arg	Lys	Arg	Ser	Pro	Thr	Glu	Ser	Val	
		50				55					60					
AAT	ACC	CCA	GTT	GGC	AAG	GAT	CCT	GGC	CTA	GCT	GGG	CGG	GGG	GAC	CCA	238
Asn	Thr	Pro	Val	Gly	Lys	Asp	Pro	Gly	Leu	Ala	Gly	Arg	Gly	Asp	Pro	
	65				70			75								
AAG	GCT	ATG	GCA	CAA	CTG	AGA	GTT	CCA	CAA	CTG	GGA	CCT	CGG	GCA	CCA	286
Lys	Ala	Met	Ala	Gln	Leu	Arg	Val	Pro	Gln	Leu	Gly	Pro	Arg	Ala	Pro	
80				85				90						95		
AGT	GCC	ACA	GGA	AAG	GGT	CCT	AAG	GAA	CTG	GAC	ACC	AGA	AGT	TTA	AAG	334
Ser	Ala	Thr	Gly	Lys	Gly	Pro	Lys	Glu	Leu	Asp	Thr	Arg	Ser	Leu	Lys	
				100				105						110		
GAA	GAA	AAT	TTT	ATA	GCA	TCT	ATT	GGG	CCT	GAA	GTA	ATC	AAA	CCT	GTC	382
Glu	Glu	Asn	Phe	Ile	Ala	Ser	Ile	Gly	Pro	Glu	Val	Ile	Lys	Pro	Val	
			115					120				125				
TTT	GAC	CTT	GGT	GAG	ACA	GAG	GAG	AAA	AAG	TCC	CAG	ATC	AGC	GCA	GAC	430
Phe	Asp	Leu	Gly	Glu	Thr	Glu	Glu	Lys	Lys	Ser	Gln	Ile	Ser	Ala	Asp	
		130				135					140					

AGT Ser	GGT Gly	GTG Val	AGC Ser	CTG Leu	ACG Thr	TCT Ser	AGT Ser	TCC Ser	CAG Gln	AGG Arg	ACT Thr	GAT Asp	CAA Gln	GAC Asp	TCT Ser	478
145						150					155					
GTC Val	ATC Ile	GGC Gly	GTG Val	AGT Ser	CCA Pro	GCT Ala	GTT Val	ATG Met	ATC Ile	CGC Arg	AGC Ser	TCA Ser	AGT Ser	CAG Gln	GAT Asp	526
160					165					170					175	
TCT Ser	GAA Glu	GTT Val	AGC Ser	ACC Thr	GTG Val	GTG Val	AGT Ser	AAT Asn	AGC Ser	TCT Ser	GGA Gly	GAG Glu	ACC Thr	CTT Leu	GGA Gly	574
				180					185					190		
GCT Ala	GAC Asp	AGT Ser	GAC Asp	TTG Leu	AGC Ser	AGC Ser	AAT Asn	GCA Ala	GGT Gly	GAT Asp	GGA Gly	CCA Pro	GGT Gly	GGC Gly	GAG Glu	622
			195					200				205				
GGC Gly	AGT Ser	GTT Val	CAC His	CTG Leu	GCA Ala	AGC Ser	TCT Ser	CGG Arg	GGC Gly	ACT Thr	TTG Leu	TCT Ser	GAT Asp	AGT Ser	GAA Glu	670
		210					215				220					
ATT Ile	GAG Glu	ACC Thr	AAC Asn	TCT Ser	GCC Ala	ACA Thr	AGC Ser	ACC Thr	ATC Ile	TTT Phe	GGT Gly	AAA Lys	GCC Ala	CAC His	AGC Ser	718
	225				230					235						
TTG Leu	AAG Lys	CCA Pro	AGC Ser	ATA Ile	AAG Lys	GAG Glu	AAG Lys	CTG Leu	GCA Ala	GGC Gly	AGC Ser	CCC Pro	ATT Ile	CGT Arg	ACT Thr	766
240				245						250				255		
TCT Ser	GAA Glu	GAT Asp	GTG Val	AGC Ser	CAG Gln	CGA Arg	GTC Val	TAT Tyr	CTC Leu	TAT Tyr	GAG Glu	GGA Gly	CTC Leu	CTA Leu	GGC Gly	814
			260					265					270			
AAA Lys	GAG Glu	CGT Arg	TCT Ser	ACT Thr	TTA Leu	TGG Trp	GAC Asp	CAA Gln	ATG Met	CAA Gln	TTC Phe	TGG Trp	GAA Glu	GAT Asp	GCC Ala	862
			275					280				285				
TTC Phe	TTA Leu	GAT Asp	GCT Ala	GTG Val	ATG Met	TTG Leu	GAG Glu	AGA Arg	GAA Glu	GGG Gly	ATG Met	GGT Gly	ATG Met	GAC Asp	CAG Gln	910
	290						295				300					
GGT Gly	CCC Pro	CAG Gln	GAA Glu	ATG Met	ATC Ile	GAC Asp	AGG Arg	TAC Tyr	CTG Leu	TCC Ser	CTT Leu	GGA Gly	GAA Glu	CAT His	GAC Asp	958
	305					310					315					
CGG Arg	AAG Lys	CGC Arg	CTG Leu	GAA Glu	GAT Asp	GAT Asp	GAA Glu	GAT Asp	CGC Arg	TTG Leu	CTG Leu	GCC Ala	ACA Thr	CTT Leu	CTG Leu	1006
320					325					330					335	
CAC His	AAC Asn	CTC Leu	ATC Ile	TCC Ser	TAC Tyr	ATG Met	CTG Leu	CTG Leu	ATG Met	AAG Lys	GTA Val	AAT Asn	AAG Lys	AAT Asn	GAC Asp	1054
			340						345				350			
ATC Ile	CGC Arg	AAG Lys	AAG Lys	GTG Val	AGG Arg	CGC Arg	CTA Leu	ATG Met	GGA Gly	AAG Lys	TCG Ser	CAC His	ATT Ile	GGG Gly	CTT Leu	1102
			355				360					365				
GTG Val	TAC Tyr	AGC Ser	CAG Gln	CAA Gln	ATC Ile	AAT Asn	GAG Glu	GTG Val	CTT Leu	GAT Asp	CAG Gln	CTG Leu	GCG Ala	AAC Asn	CTG Leu	1150
		370					375					380				
AAT Asn	GGA Gly	CGC Arg	GAT Asp	CTC Leu	TCT Ser	ATC Ile	TGG Trp	TCC Ser	AGT Ser	GGC Gly	AGC Ser	CGG Arg	CAC His	ATG Met	AAG Lys	1198
	385					390										

TTT TTC ATG GAG GTG TGC GAT GAC TGT GTG GTG TTG CGT AGT AAC ATC Phe Phe Met Glu Val Cys Asp Asp Cys Val Val Leu Arg Ser Asn Ile 420 425 430	1294
GGA ACA GTG TAT GAG CGC TGG TGG TAC GAG AAG CTC ATC AAC ATG ACC Gly Thr Val Tyr Glu Arg Trp Trp Tyr Glu Lys Leu Ile Asn Met Thr 435 440 445	1342
TAC TGT CCC AAG ACG AAG GTG TTG TGC TTG TGG CGT AGA AAT GGC TCT Tyr Cys Pro Lys Thr Lys Val Leu Cys Leu Trp Arg Arg Asn Gly Ser 450 455 460	1390
GAG ACC CAG CTC AAC AAG TTC TAT ACT AAA AAG TGT CGG GAG CTG TAC Glu Thr Gln Leu Asn Lys Phe Tyr Thr Lys Lys Cys Arg Glu Leu Tyr 465 470 475	1438
TAC TGT GTG AAG GAC AGC ATG GAG CGC GCT GCC GCC CGA CAG CAA AGC Tyr Cys Val Lys Asp Ser Met Glu Arg Ala Ala Ala Arg Gln Gln Ser 480 485 490 495	1486
ATC AAA CCC GGA CCT GAA TTG GGT GGC GAG TTC CCT GTG CAG GAC CTG Ile Lys Pro Gly Pro Glu Leu Gly Gly Glu Phe Pro Val Gln Asp Leu 500 505 510	1534
AAG ACT GGT GAG GGT GGC CTG CTG CAG GTG ACC CTG GAA GGG ATC AAC Lys Thr Gly Glu Gly Gly Leu Leu Gln Val Thr Leu Glu Gly Ile Asn 515 520 525	1582
CTC AAA TTC ATG CAC AAT CAG GTT TTC ATA GAG CTG AAT CAC ATT AAA Leu Lys Phe Met His Asn Gln Val Phe Ile Glu Leu Asn His Ile Lys 530 535 540	1630
AAG TGC AAT ACA GTT CGA GGC GTC TTT GTC CTG GAG GAA TTT GTT CCT Lys Cys Asn Thr Val Arg Gly Val Phe Val Leu Glu Glu Phe Val Pro 545 550 555	1678
GAA ATT AAA GAA GTG GTG AGC CAC AAG TAC AAG ACA CCA ATG GCC CAC Glu Ile Lys Glu Val Val Ser His Lys Tyr Lys Thr Pro Met Ala His 560 565 570 575	1726
GAA ATC TGC TAC TCC GTA TTA TGT CTC TTC TCG TAC GTG GCT GCA GTT Glu Ile Cys Tyr Ser Val Leu Cys Leu Phe Ser Tyr Val Ala Ala Val 580 585 590	1774
CAT AGC AGT GAG GAA GAT CTC AGA ACC CCG CCC CGG CCT GTC TCT AGC His Ser Ser Glu Glu Asp Leu Arg Thr Pro Pro Arg Pro Val Ser Ser 595 600 605	1822
TGATGGAGAG GGGCTACGCA GCTGCCCCAG CCCAGGGCAC GCCCCTGGCC CCTTGCTGTT	1882
CCCAAGTGCA CGATGCTGCT GTGACTGAGG AGTGGATGAT GCTCGTGTGT CCTCTGCAAG	1942
CCCCCTGCTG TGGCTTGGTT GGTACCAGT TATGTGTCCC TCTGAGTGTG TCTTGAGCGT	2002
GTCCACCTTC TCCCTCTCCA CTCCCAGAAG ACCAAACTGC CTTCCCCTCA GGGCTCAAGA	2062
ATGTGTACAG TCTGTGGGGC CGGTGTGAAC CCACTATTTT GTGTCCTGA GACATTGTG	2122
TTGTGGTTCC TTGTCCTTGT CCCTGGCGTT ATAAGTGTCC ACTGCAAGAG TCTGGCTCTC	2182
CCTTCTCTGT GACCCGGCAT GACTGGGCGC CTGGAGCAGT TTTACTCTGT GAGGAGTGAG	2242
GGAAACCCTGG GGCTCACCCCT CTCAGAGGAA GGGCACAGAG AGGAAGGGAA GAATTGGGGG	2302
GCAGCCGGAG TGAGTGGCAG CCTCCCTGCT TCCTTCTGCA TTCCCAAGCC GGCAGCTACT	2362
GCCCAGGGCC CGCAGTGTG GCTGCTGCCT GCCACAGCCT CTGTGACTGC AGTGGAGCGG	2422

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225		230		235		240
Lys Pro Ser Ile	Lys Glu Lys Leu Ala Gly	Ser Pro Ile Arg Thr Ser				
	245	250	255			
Glu Asp Val Ser	Gln Arg Val Tyr Leu Tyr Glu Gly Leu Leu Gly Lys					
	260	265	270			
Glu Arg Ser Thr	Leu Trp Asp Gln Met Gln Phe Trp Glu Asp Ala Phe					
	275	280	285			
Leu Asp Ala Val	Met Leu Glu Arg Glu Gly Met Gly Met Asp Gln Gly					
	290	295	300			
Pro Gln Glu Met	Ile Asp Arg Tyr Leu Ser Leu Gly Glu His Asp Arg					
	305	310	315			320
Lys Arg Leu Glu	Asp Asp Glu Asp Arg Leu Leu Ala Thr Leu Leu His					
	325	330				335
Asn Leu Ile Ser	Tyr Met Leu Leu Met Lys Val Asn Lys Asn Asp Ile					
	340	345	350			
Arg Lys Lys Val	Arg Arg Leu Met Gly Lys Ser His Ile Gly Leu Val					
	355	360	365			
Tyr Ser Gln Gln	Ile Asn Glu Val Leu Asp Gln Leu Ala Asn Leu Asn					
	370	375	380			
Gly Arg Asp Leu	Ser Ile Trp Ser Ser Gly Ser Arg His Met Lys Lys					
	385	390	395			400
Gln Thr Phe Val	Val His Ala Gly Thr Asp Thr Asn Gly Asp Ile Phe					
	405	410	415			
Phe Met Glu Val	Cys Asp Asp Cys Val Val Leu Arg Ser Asn Ile Gly					
	420	425	430			
Thr Val Tyr Glu	Arg Trp Trp Tyr Glu Lys Leu Ile Asn Met Thr Tyr					
	435	440	445			
Cys Pro Lys Thr	Lys Val Leu Cys Leu Trp Arg Arg Asn Gly Ser Glu					
	450	455	460			
Thr Gln Leu Asn	Lys Phe Tyr Thr Lys Lys Cys Arg Glu Leu Tyr Tyr					
	465	470	475			480
Cys Val Lys Asp	Ser Met Glu Arg Ala Ala Arg Gln Gln Ser Ile					
	485	490	495			
Lys Pro Gly Pro	Glu Leu Gly Gly Glu Phe Pro Val Gln Asp Leu Lys					
	500	505	510			
Thr Gly Glu Gly	Gly Leu Leu Gln Val Thr Leu Glu Gly Ile Asn Leu					
	515	520	525			
Lys Phe Met His	Asn Gln Val Phe Ile Glu Leu Asn His Ile Lys Lys					
	530	535	540			
Cys Asn Thr Val	Arg Gly Val Phe Val Leu Glu Glu Phe Val Pro Glu					
	545	550	555			560
Ile Lys Glu Val	Val Ser His Lys Tyr Lys Thr Pro Met Ala His Glu					
	565	570	575			
Ile Cys Tyr Ser	Val Leu Cys Leu Phe Ser Tyr Val Ala Ala Val His					
	580	585	590			

DECEMBER 1, 1960

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3225 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(iii) HYPOTHETICAL: NO

(A) NAME/KEY: CDS
(B) LOCATION: 3..2846

CC	CAG	ACT	CGC	CCC	GCC	CCA	GAG	ACT	GCG	CCT	GCG	CGG	GCA	CGA	GAC	47
	Gln	Thr	Arg	Pro	Ala	Pro	Glu	Thr	Ala	Pro	Ala	Arg	Ala	Arg	Asp	
	1				5				10						15	
ACC	CTC	TCC	GCG	ATG	ACT	GCC	AGC	TCA	GTG	GAG	CAG	CTG	CGG	AAG	GAG	95
Thr	Leu	Ser	Ala	Met	Thr	Ala	Ser	Ser	Val	Glu	Gln	Leu	Arg	Lys	Glu	
				20					25					30		
GGC	AAT	GAG	CTG	TTC	AAA	TGT	GGA	GAC	TAC	GGG	GGC	GCC	CTG	GCG	GCC	143
Gly	Asn	Glu	Leu	Phe	Lys	Cys	Gly	Asp	Tyr	Gly	Gly	Ala	Leu	Ala	Ala	
			35					40					45			
TAC	ACT	CAG	GCC	CTG	GGT	CTG	GAC	GCG	ACG	CCC	CAG	GAC	CAG	GCC	GTT	191
Tyr	Thr	Gln	Ala	Leu	Gly	Leu	Asp	Ala	Thr	Pro	Gln	Asp	Gln	Ala	Val	
		50					55					60				
CTG	CAC	CGG	AAC	CGG	GCC	GCC	TGC	CAC	CTC	AAG	CTG	GAA	GAT	TAC	GAC	239
Leu	His	Arg	Asn	Arg	Ala	Ala	Cys	His	Leu	Lys	Leu	Glu	Asp	Tyr	Asp	
	65					70					75					
AAA	GCA	GAA	ACA	GAG	GCA	TCC	AAA	GCC	ATT	GAA	AAG	GAT	GGT	GGG	GAT	287
Lys	Ala	Glu	Thr	Glu	Ala	Ser	Lys	Ala	Ile	Glu	Lys	Asp	Gly	Gly	Asp	
	80				85					90					95	
GTC	AAA	GCA	CTC	TAC	CGG	CGG	AGC	CAA	GCC	CTA	GAG	AAG	CTG	GGC	CGC	335
Val	Lys	Ala	Leu	Tyr	Arg	Arg	Ser	Gln	Ala	Leu	Glu	Lys	Leu	Gly	Arg	
				100					105					110		
CTG	GAC	CAG	GCT	GTC	CTT	GAC	CTG	CAG	AGA	TGT	GTG	AGC	TTG	GAG	CCC	383
Leu	Asp	Gln	Ala	Val	Leu	Asp	Leu	Gln	Arg	Cys	Val	Ser	Leu	Glu	Pro	
			115					120					125			
AAG	AAC	AAA	GTT	TTC	CAG	GAG	GCC	TTG	CGG	AAC	ATC	GGG	GGC	CAG	ATT	431
Lys	Asn	Lys	Val	Phe	Gln	Glu	Ala	Leu	Arg	Asn	Ile	Gly	Gly	Gln	Ile	
		130					135					140				
CAG	GAG	AAG	GTG	CGA	TAC	ATG	TCC	TCG	ACG	GAT	GCC	AAA	GTG	GAA	CAG	479
Gln	Glu	Lys	Val	Arg	Tyr	Met	Ser	Ser	Thr	Asp	Ala	Lys	Val	Glu	Gln	
	145					150					155					

ATG TTT CAG ATA CTG TTG GAC CCA GAA GAG AAG GGC ACT GAG AAA AAG Met Phe Gln Ile Leu Leu Asp Pro Glu Glu Lys Gly Thr Glu Lys Lys 160 165 170 175	527
CAA AAG GCT TCT CAG AAC CTG GTG GTG CTG GCC AGG GAG GAT GCT GGA Gln Lys Ala Ser Gln Asn Leu Val Val Leu Ala Arg Glu Asp Ala Gly 180 185 190	575
GCG GAG AAG ATC TTC CGG AGT AAT GGG GTT CAG CTC TTG CAA CGT TTA Ala Glu Lys Ile Phe Arg Ser Asn Gly Val Gln Leu Leu Gln Arg Leu 195 200 205	623
CTG GAC ATG GGA GAG ACT GAC CTC ATG CTG GCG GCT CTG CGT ACG CTG Leu Asp Met Gly Glu Thr Asp Leu Met Leu Ala Ala Leu Arg Thr Leu 210 215 220	671
GTT GGC ATT TGC TCT GAG CAT CAG TCA CGG ACA GTG GCA ACC CTG AGC Val Gly Ile Cys Ser Glu His Gln Ser Arg Thr Val Ala Thr Leu Ser 225 230 235	719
ATA CTG GGA ACT CGG CGA GTA GTC TCC ATC CTG GGC GTG GAA AGC CAG Ile Leu Gly Thr Arg Arg Val Val Ser Ile Leu Gly Val Glu Ser Gln 240 245 250 255	767
GCT GTG TCC CTG GCT GCC TGC CAC CTG CTG CAG GTT ATG TTT GAT GCC Ala Val Ser Leu Ala Ala Cys His Leu Leu Gln Val Met Phe Asp Ala 260 265 270	815
CTC AAG GAA GGT GTC AAA AAA GGC TTC CGA GGC AAA GAA GGT GCC ATC Leu Lys Glu Gly Val Lys Lys Gly Phe Arg Gly Lys Glu Gly Ala Ile 275 280 285	863
ATT GTG GAT CCT GCC CGG GAG CTG AAG GTC CTC ATC AGT AAC CTC TTA Ile Val Asp Pro Ala Arg Glu Leu Lys Val Leu Ile Ser Asn Leu Leu 290 295 300	911
GAT CTG CTG ACA GAG GTG GGG GTC TCT GGC CAA GGC CGA GAC AAT GCC Asp Leu Leu Thr Glu Val Lys Val Ser Gly Gln Gly Arg Asp Asn Ala 305 310 315	959
CTG ACC CTC CTG ATT AAA GCG GTG CCC CGG AAG TCT CTC AAG GAC CCC Leu Thr Leu Leu Ile Lys Ala Val Pro Arg Lys Ser Leu Lys Asp Pro 320 325 330 335	1007
AAC AAC AGC CTC ACC CTC TGG GTC ATC GAC CAA GGT CTG AAA AAG ATT Asn Asn Ser Leu Thr Leu Trp Val Ile Asp Gln Gly Leu Lys Lys Ile 340 345 350	1055
TTG GAA GTG GGG GGC TCT CTA CAG GAC CCT CCT GGG GAG CTC GCA GTG Leu Glu Val Gly Gly Ser Leu Gln Asp Pro Pro Gly Glu Leu Ala Val 355 360 365	1103
ACC GCA AAC AGC CGC ATG AGC GCC TCT ATT CTC CTC AGC AAG CTC TTT Thr Ala Asn Ser Arg Met Ser Ala Ser Ile Leu Leu Ser Lys Leu Phe 370 375 380	1151
GAT GAC CTC AAG TGT GAT GCG GAG AGG GAG AAT TTC CAC AGA CTT TGT Asp Asp Leu Lys Cys Asp Ala Glu Arg Glu Asn Phe His Arg Leu Cys 385 390 395	1199
GAA AAC TAC ATC AAG AGC TGG TTT GAG GGC CAA GGG CTG GCC GGG AAG Glu Asn Tyr Ile Lys Ser Trp Phe Glu Gly Gln Gly Leu Ala Gly Lys 400 405 410 415	1247
CTA CGG GCC ATC CAG ACG GTG TCC TGC CTC CTG CAG GGC CCA TGT GAC Leu Arg Ala Ile Gln Thr Val Ser Cys Leu Leu Gln Gly Pro Cys Asp 420 425 430	1295

GCT Ala	GGC Gly	AAC Asn	CGG Arg 435	GCC Ala	TTG Leu	GAG Glu	CTG Leu	AGC Ser 440	GGT Gly	GTC Val	ATG Met	GAG Glu	AGT Ser 445	GTG Val	ATT Ile	1343
GCT Ala	CTG Leu	TGT Cys 450	GCC Ala	TCT Ser	GAG Glu	CAG Gln	GAG Glu 455	GAG Glu	GAG Glu	CAG Gln	CTG Leu	GTG Val 460	GCC Ala	GTG Val	GAG Glu	1391
GCT Ala	CTG Leu 465	ATC Ile	CAT His	GCA Ala	GCC Ala	GGC Gly 470	AAG Lys	GCT Ala	AAG Lys	CGG Arg	GCC Ala 475	TCA Ser	TTC Phe	ATC Ile	ACT Thr	1439
GCC Ala 480	AAT Asn	GGT Gly	GTC Val	TCG Ser	CTG Leu 485	CTG Leu	AAG Lys	GAC Asp	CTA Leu	TAT Tyr 490	AAG Lys	TGC Cys	AGC Ser	GAG Glu	AAG Lys 495	1487
GAC Asp	AGC Ser	ATC Ile	CGC Arg 500	ATC Ile	CGG Arg	GCG Ala	CTA Leu	GTG Val	GGA Gly 505	CTC Leu	TGT Cys	AAG Lys	CTC Leu	GGT Gly 510	TCG Ser	1535
GCT Ala	GGA Gly	GGG Gly	ACT Thr 515	GAC Asp	TTC Phe	AGC Ser	ATG Met	AAG Lys 520	CAG Gln	TTT Phe	GCT Ala	GAA Glu	GGC Gly 525	TCC Ser	ACT Thr	1583
CTC Leu	AAA Lys	CTG Leu 530	GCT Ala	AAG Lys	CAG Gln	TGT Cys	CGA Arg 535	AAG Lys	TGG Trp	CTG Leu	TGC Cys	AAT Asn 540	GAC Asp	CAG Gln	ATC Ile	1631
GAC Asp	GCA Ala 545	GGC Gly	ACT Thr	CGG Arg	CGC Arg	TGG Trp 550	GCA Ala	GTG Val	GAG Glu	GGC Gly	CTG Leu 555	GCT Ala	TAC Tyr	CTG Leu	ACC Thr	1679
TTT Phe 560	GAT Asp	GCC Ala	GAC Asp	GTG Val	AAG Lys 565	GAA Glu	GAG Glu	TTT Phe	GTG Val	GAG Glu 570	GAT Asp	GCG Ala	GCT Ala	GCT Ala	CTG Leu 575	1727
AAA Lys	GCT Ala	CTG Leu	TTC Phe	CAG Gln 580	CTC Leu	AGC Ser	AGG Arg	TTG Leu	GAG Glu 585	GAG Glu	AGG Arg	TCA Ser	GTG Val	CTC Leu 590	TTT Phe	1775
GCG Ala	GTG Val	GCC Ala	TCA Ser 595	GCG Ala	CTG Leu	GTG Val	AAC Asn 600	TGC Cys	ACC Thr	AAC Asn	AGC Ser	TAT Tyr	GAC Asp 605	TAC Tyr	GAG Glu	1823
GAG Glu	CCC Pro 610	GAC Asp	CCC Pro	AAG Lys	ATG Met	GTG Val	GAG Glu 615	CTG Leu	GCC Ala	AAG Lys	TAT Tyr 620	GCC Ala	AAG Lys	CAG Gln	CAT His	1871
GTG Val	CCC Pro 625	GAG Glu	CAG Gln	CAC His	CCC Pro	AAG Lys 630	GAC Asp	AAG Lys	CCA Pro	AGC Ser	TTC Phe 635	GTG Val	CGG Arg	GCT Ala	CGG Arg	1919
GTG Val 640	AAG Lys	AAG Lys	CTG Leu	CTG Leu	GCA Ala 645	GCG Ala	GGT Gly	GTG Val	GTG Val	TCG Ser 650	GCC Ala	ATG Met	GTG Val	TGC Cys	ATG Met 655	1967
GTG Val	AAG Lys	ACG Thr	GAG Glu	AGC Ser 660	CCT Pro	GTG Val	CTG Leu	ACC Thr	AGT Ser 665	TCC Ser	TGC Cys	AGA Arg	GAG Glu	CTG Leu 670	CTC Leu	2015
TCC Ser	AGG Arg	GTC Val	TTC Phe 675	TTG Leu	GCT Ala	TTA Leu	GTG Val	GAA Glu 680	GAG Glu	GTA Val	GAG Glu	GAC Asp	CGA Arg 685	GGC Gly	ACT Thr	2063
GTG Val	GTT Val	GCC Ala 690	CAG Gln	GGA Gly	GGC Gly	GGC Gly	AGG Arg 695	GCG Ala	CTG Leu	ATC Ile	CCG Pro 700	CTG Leu	GCC Ala	CTG Leu	GAA Glu	2111

GGC Gly	ACG Thr	GAC Asp	GTG Val	GGG Gly	CAG Gln	ACA Thr	AAG Lys	GCA Ala	GCC Ala	CAG Gln	GCC Ala	CTT Leu	GCC Ala	AAG Lys	CTC Leu	2159
ACC Thr	ATC Ile	ACC Thr	TCC Ser	AAC Asn	CCG Pro	GAG Glu	ATG Met	ACC Thr	TTC Phe	CCT Pro	GGC Gly	GAG Glu	CGG Arg	ATC Ile	TAT Tyr	2207
GAG Glu	GTG Val	GTC Val	CGG Arg	CCC Pro	CTC Leu	GTC Val	TCC Ser	CTG Leu	TTG Leu	CAC His	CTC Leu	AAC Asn	TGC Cys	TCA Ser	GGC Gly	2255
CTG Leu	CAG Gln	AAC Asn	TTC Phe	GAG Glu	GCG Ala	CTC Leu	ATG Met	GCC Ala	CTA Leu	ACA Thr	AAC Asn	CTG Leu	GCT Ala	GGG Gly	ATC Ile	2303
AGC Ser	GAG Glu	AGG Arg	CTC Leu	CGG Arg	CAG Gln	AAG Lys	ATC Ile	CTG Leu	AAG Lys	GAG Glu	AAG Lys	GCT Ala	GTG Val	CCC Pro	ATG Met	2351
ATA Ile	GAA Glu	GGC Gly	TAC Tyr	ATG Met	TTT Phe	GAG Glu	GAG Glu	CAT His	GAG Glu	ATG Met	ATC Ile	CGC Arg	CGG Arg	GCA Ala	GCC Ala	2399
ACG Thr	GAG Glu	TGC Cys	ATG Met	TGT Cys	AAC Asn	TTG Leu	GCC Ala	ATG Met	AGC Ser	AAG Lys	GAG Glu	GTG Val	CAG Gln	GAC Asp	CTC Leu	2447
TTC Phe	GAA Glu	GCC Ala	CAG Gln	GGC Gly	AAT Asn	GAC Asp	CGA Arg	CTG Leu	AAG Lys	CTG Leu	CTG Leu	GTG Val	CTG Leu	TAC Tyr	AGT Ser	2495
GGA Gly	GAG Glu	GAT Asp	GAT Asp	GAG Glu	CTG Leu	CTA Leu	CAG Gln	CGG Arg	GCA Ala	GCT Ala	GCC Ala	GGG Gly	GGC Gly	TTG Leu	GCC Ala	2543
ATG Met	CTT Leu	ACC Thr	TCC Ser	ATG Met	CGG Arg	CCC Pro	ACG Thr	CTC Leu	TGC Cys	AGC Ser	CGC Arg	ATT Ile	CCC Pro	CAA Gln	GTG Val	2591
ACC Thr	ACA Thr	CAC His	TGG Trp	CTG Leu	GAG Glu	ATC Ile	CTG Leu	CAG Gln	GCC Ala	CTG Leu	CTT Leu	CTG Leu	AGC Ser	TCC Ser	AAC Asn	2639
CAG Gln	GAG Glu	CTG Leu	CAG Gln	CAC His	CGG Arg	GGT Gly	GCT Ala	GTG Val	GTG Val	GTG Val	CTG Leu	AAC Asn	ATG Met	GTG Val	GAG Glu	2687
GCC Ala	TCG Ser	AGG Arg	GAG Glu	ATT Ile	GCC Ala	AGC Ser	ACC Thr	CTG Leu	ATG Met	GAG Glu	AGT Ser	GAG Glu	ATG Met	ATG Met	GAG Glu	2735
ATC Ile	TTG Leu	TCA Ser	GTG Val	CTA Leu	GCT Ala	AAG Lys	GGT Gly	GAC Asp	CAC His	AGC Ser	CCT Pro	GTC Val	ACA Thr	AGG Arg	GCT Ala	2783
GCT Ala	GCA Ala	GCC Ala	TGC Cys	CTG Leu	GAC Asp	AAA Lys	GCA Ala	GTG Val	GAA Glu	TAT Tyr	GGG Gly	CTT Leu	ATC Ile	CAA Gln	CCC Pro	2831
AAC Asn	CAA Gln	GAT Asp	GGA Gly	GAG Glu	TGAGGGGGTT	GTCCCTGGGC	CCAAGGCTCA	TGCACACGCT								2886
ACCTATTGTG GCACGGAGAG TAAGGACGGA AGCAGCTTTG GCTGGTG GTGCTGGCATGC																2946
CCAATACTCT TGCCCCATCCT CGCTTGCTGC CCTAGGATGT CCTCTGTTCT GAGTCAGCGG																3006

Val Ser Leu Ala Ala Cys His Leu Leu Gln Val Met Phe Asp Ala Leu
260 265 270

Lys Glu Gly Val Lys Lys Gly Phe Arg Gly Lys Glu Gly Ala Ile Ile
275 280 285

Val Asp Pro Ala Arg Glu Leu Lys Val Leu Ile Ser Asn Leu Leu Asp
290 295 300

Leu Leu Thr Glu Val Gly Val Ser Gly Gln Gly Arg Asp Asn Ala Leu
305 310 315 320

Thr Leu Leu Ile Lys Ala Val Pro Arg Lys Ser Leu Lys Asp Pro Asn
325 330 335

Asn Ser Leu Thr Leu Trp Val Ile Asp Gln Gly Leu Lys Lys Ile Leu
340 345 350

Glu Val Gly Gly Ser Leu Gln Asp Pro Pro Gly Glu Leu Ala Val Thr
355 360 365

Ala Asn Ser Arg Met Ser Ala Ser Ile Leu Leu Ser Lys Leu Phe Asp
370 375 380

Asp Leu Lys Cys Asp Ala Glu Arg Glu Asn Phe His Arg Leu Cys Glu
385 390 395 400

Asn Tyr Ile Lys Ser Trp Phe Glu Gly Gln Gly Leu Ala Gly Lys Leu
405 410 415

Arg Ala Ile Gln Thr Val Ser Cys Leu Leu Gln Gly Pro Cys Asp Ala
420 425 430

Gly Asn Arg Ala Leu Glu Leu Ser Gly Val Met Glu Ser Val Ile Ala
435 440 445

Leu Cys Ala Ser Glu Gln Glu Glu Glu Gln Leu Val Ala Val Glu Ala
450 455 460

Leu Ile His Ala Ala Gly Lys Ala Lys Arg Ala Ser Phe Ile Thr Ala
465 470 475 480

Asn Gly Val Ser Leu Leu Lys Asp Leu Tyr Lys Cys Ser Glu Lys Asp
485 490 495

Ser Ile Arg Ile Arg Ala Leu Val Gly Leu Cys Lys Leu Gly Ser Ala
500 505 510

Gly Gly Thr Asp Phe Ser Met Lys Gln Phe Ala Glu Gly Ser Thr Leu
515 520 525

Lys Leu Ala Lys Gln Cys Arg Lys Trp Leu Cys Asn Asp Gln Ile Asp
530 535 540

Ala Gly Thr Arg Arg Trp Ala Val Glu Gly Leu Ala Tyr Leu Thr Phe
545 550 555 560

Asp Ala Asp Val Lys Glu Glu Phe Val Glu Asp Ala Ala Ala Leu Lys
565 570 575

Ala Leu Phe Gln Leu Ser Arg Leu Glu Glu Arg Ser Val Leu Phe Ala
580 585 590

Val Ala Ser Ala Leu Val Asn Cys Thr Asn Ser Tyr Asp Tyr Glu Glu
595 600 605

Pro Asp Pro Lys Met Val Glu Leu Ala Lys Tyr Ala Lys Gln His Val

[illegible]

(2) INFORMATION FOR SEQ ID NO:15:

SECRET

(iii) HYPOTHETICAL: NO

(A) NAME/KEY: CDS
(B) LOCATION: 326..5092

CACGTGCATG	TGTAGCATGC	CTTGGTTTTT	CCTTTGGCAT	CTGAAAAAGG	CACAACCTGA		60										
AAGACCTAGA	ACCCAGTGTC	GGTCCCCAGG	CCCTTTGGGA	CAGGAAGAGA	AGAGCCCGTG		120										
GGCCGCGGGG	AGGATGTCCT	GCGGCGGGGC	TGTCCTCGCG	GACTGACTGG	ACTCCATCTC		180										
CCAGCGGGCG	CCGCGGCGCG	GCCACGCCCC	CCCACTCCCC	GCGCGCGCCC	GGTGGAGACT		240										
TCGATTTTCA	GAATTCCTCC	TGGGAATGCT	GACTCCTTGC	TTGGTGCCCT	GATGCTTCTC		300										
TGAGATAAAC	TGATGAATTG	GAACC	ATG	GTG	CAA	AAG	AAG	AAG	TTC	TGT	CCT		352				
			Met	Val	Gln	Lys	Lys	Lys	Phe	Cys	Pro						
			1					5									
CGG	TTA	CTT	GAC	TAT	CTA	GTG	ATC	GTA	GGG	GCC	AGG	CAC	CCG	AGC	AGT		400
Arg	Leu	Leu	Asp	Tyr	Leu	Val	Ile	Val	Gly	Ala	Arg	His	Pro	Ser	Ser		
10					15					20					25		
GAT	AGC	GTG	GCC	CAG	ACT	CCT	GAA	TTG	CTA	CGG	CGA	TAC	CCC	TTG	GAG		448
Asp	Ser	Val	Ala	Gln	Thr	Pro	Glu	Leu	Leu	Arg	Arg	Tyr	Pro	Leu	Glu		
				30					35					40			
GAT	CAC	ACT	GAG	TTT	CCC	CTG	CCC	CCA	GAT	GTA	GTG	TTC	TTC	TGC	CAG		496
Asp	His	Thr	Glu	Phe	Pro	Leu	Pro	Pro	Asp	Val	Val	Phe	Phe	Cys	Gln		
			45					50					55				
CCC	GAG	GGC	TGC	CTG	AGC	GTG	CGG	CAG	CGG	CGC	ATG	AGC	CTT	CGG	GAT		544
Pro	Glu	Gly	Cys	Leu	Ser	Val	Arg	Gln	Arg	Arg	Met	Ser	Leu	Arg	Asp		
		60					65					70					
GAT	ACC	TCT	TTT	GTC	TTC	ACC	CTC	ACT	GAC	AAG	GAC	ACT	GGA	GTC	ACG		592
Asp	Thr	Ser	Phe	Val	Phe	Thr	Leu	Thr	Asp	Lys	Asp	Thr	Gly	Val	Thr		
	75					80					85						
CGA	TAT	GGC	ATC	TGT	GTT	AAC	TTC	TAC	CGC	TCC	TTC	CAA	AAG	CGA	ATC		640
Arg	Tyr	Gly	Ile	Cys	Val	Asn	Phe	Tyr	Arg	Ser	Phe	Gln	Lys	Arg	Ile		
90					95					100					105		
TCT	AAG	GAG	AAG	GGG	GAA	GGT	GGG	GCA	GGG	TCC	CGT	GGG	AAG	GAA	GGA		688
Ser	Lys	Glu	Lys	Gly	Glu	Gly	Gly	Ala	Gly	Ser	Arg	Gly	Lys	Glu	Gly		
				110					115					120			
ACC	CAT	GCC	ACC	TGT	GCC	TCA	GAA	GAG	GGT	GGC	ACT	GAG	AGC	TCA	GAG		736
Thr	His	Ala	Thr	Cys	Ala	Ser	Glu	Glu	Gly	Gly	Thr	Glu	Ser	Ser	Glu		
			125					130					135				
AGT	GGC	TCA	TCC	CTG	CAG	CCT	CTC	AGT	GCT	GAC	TCT	ACC	CCT	GAT	GTG		784
Ser	Gly	Ser	Ser	Leu	Gln	Pro	Leu	Ser	Ala	Asp	Ser	Thr	Pro	Asp	Val		
	140						145					150					

AAC Asn 155	CAG Gln	TCT Ser	CCT Pro	CGG Arg	GGC Gly	AAA Lys 160	CGC Arg	CGG Arg	GCC Ala	AAG Lys	GC Ala 165	GGG Gly	AGC Ser	CGC Arg	TCC Ser	832
CGC Arg 170	AAC Asn	AGT Ser	ACT Thr	CTC Leu	ACG Thr 175	TCC Ser	CTG Leu	TGC Cys	GTG Val	CTC Leu 180	AGC Ser	CAC His	TAC Tyr	CCT Pro	TTC Phe 185	880
TTC Phe	TCC Ser	ACC Thr	TTC Phe	CGA Arg 190	GAG Glu	TGT Cys	TTG Leu	TAT Tyr	ACT Thr 195	CTC Leu	AAG Lys	CGC Arg	CTG Leu	GTG Val 200	GAC Asp	928
TGC Cys	TGT Cys	AGT Ser	GAG Glu 205	CGC Arg	CTT Leu	CTG Leu	GGC Gly 210	AAG Lys	AAA Lys	CTG Leu	GGC Gly	ATC Ile	CCT Pro 215	CGA Arg	GGC Gly	976
GTA Val	CAA Gln	AGG Arg 220	GAC Asp	ACC Thr	ATG Met	TGG Trp	CGG Arg 225	ATC Ile	TTT Phe	ACT Thr	GGA Gly 230	TCG Ser	CTG Leu	CTG Leu	GTA Val	1024
GAG Glu 235	GAG Glu	AAG Lys	TCA Ser	AGT Ser	GCC Ala	CTT Leu 240	CTG Leu	CAT His	GAC Asp	CTT Leu 245	CGA Arg	GAG Glu	ATT Ile	GAG Glu	GCC Ala	1072
TGG Trp 250	ATC Ile	TAT Tyr	CGA Arg	TTG Leu 255	CTG Leu	CGC Arg	TCC Ser	CCA Pro	GTA Val	CCC Pro 260	GTC Val	TCT Ser	GGG Gly	CAG Gln	AAG Lys 265	1120
CGA Arg	GTA Val	GAC Asp	ATC Ile 270	GAG Glu	GTC Val	CTA Leu	CCC Pro	CAA Gln	GAG Glu 275	CTC Leu	CAG Gln	CCA Pro	GCT Ala	CTG Leu 280	ACC Thr	1168
TTT Phe	GCT Ala	CTT Leu	CCA Pro 285	GAC Asp	CCA Pro	TCT Ser	CGA Arg	TTC Phe 290	ACC Thr	CTA Leu	GTG Val	GAT Asp	TTC Phe 295	CCA Pro	CTG Leu	1216
CAC His	CTT Leu 300	CCC Pro	TTG Leu	GAA Glu	CTT Leu	CTA Leu	GGT Gly 305	GTG Val	GAC Asp	GCC Ala	TGT Cys 310	CTC Leu	CAG Gln	GTG Val	CTA Leu	1264
ACC Thr 315	TGC Cys	ATT Ile	CTG Leu	TTA Leu	GAG Glu	CAC His 320	AAG Lys	GTG Val	GTG Val	CTA Leu 325	CAG Gln	TCC Ser	CGA Arg	GAC Asp	TAC Tyr	1312
AAT Asn 330	GCA Ala	CTC Leu	TCC Ser	ATG Met	TCT Ser 335	GTG Val	ATG Met	GCA Ala	TTC Phe	GTG Val 340	GCA Ala	ATG Met	ATC Ile	TAC Tyr	CCA Pro 345	1360
CTG Leu	GAA Glu	TAT Tyr	ATG Met 350	TTT Phe	CCT Pro	GTC Val	ATC Ile	CCG Pro	CTG Leu 355	CTA Leu	CCC Pro	ACC Thr	TGC Cys	ATG Met 360	GCA Ala	1408
TCA Ser	GCA Ala	GAG Glu 365	CAG Gln	CTG Leu	CTG Leu	TTG Leu	GCT Ala	CCA Pro 370	ACC Thr	CCG Pro	TAC Tyr	ATC Ile	ATT Ile 375	GGG Gly	GTT Val	1456
CCT Pro	GCC Ala	AGC Ser 380	TTC Phe	TTC Phe	CTC Leu	TAC Tyr	AAA Lys 385	CTG Leu	GAC Asp	TTC Phe	AAA Lys	ATG Met 390	CCT Pro	GAT Asp	GAT Asp	1504
GTA Val	TGG Trp 395	CTA Leu	GTG Val	GAT Asp	CTG Leu 400	GAC Asp	AGC Ser	AAT Asn	AGG Arg	GTG Val 405	ATT Ile	GCC Ala	CCC Pro	ACC Thr	AAT Asn	1552
GCA Ala 410	GAA Glu	GTG Val	CTG Leu	CCT Pro	ATC Ile 415	CTG Leu	CCA Pro	GAA Glu	CCA Pro	GAA Glu 420	TCA Ser	CTA Leu	GAG Glu	CTG Leu	AAA Lys 425	1600

AAG CAT TTA AAG CAG GCC TTG GCC AGC ATG AGT CTC AAC ACC CAG CCC Lys His Leu Lys Gln Ala Leu Ala Ser Met Ser Leu Asn Thr Gln Pro 430 435 440	1648
ATC CTC AAT CTG GAG AAA TTT CAT GAG GGC CAG GAG ATC CCC CTT CTC Ile Leu Asn Leu Glu Lys Phe His Glu Gly Gln Glu Ile Pro Leu Leu 445 450 455	1696
TTG GGA AGG CCT TCT AAT GAC CTG CAG TCC ACA CCG TCC ACT GAA TTC Leu Gly Arg Pro Ser Asn Asp Leu Gln Ser Thr Pro Ser Thr Glu Phe 460 465 470	1744
AAC CCA CTC ATC TAT GGC AAT GAT GTG GAT TCT GTG GAT GTT GCA ACC Asn Pro Leu Ile Tyr Gly Asn Asp Val Asp Ser Val Asp Val Ala Thr 475 480 485	1792
AGG GTT GCC ATG GTA CGG TTC TTC AAT TCC GCC AAC GTG CTG CAG GGA Arg Val Ala Met Val Arg Phe Phe Asn Ser Ala Asn Val Leu Gln Gly 490 495 500 505	1840
TTT CAG ATG CAC ACG CGT ACC CTG CGC CTC TTT CCT CGG CCT GTG GTA Phe Gln Met His Thr Arg Thr Leu Arg Leu Phe Pro Arg Pro Val Val 510 515 520	1888
GCT TTT CAA GCT GGC TCC TTT CTA GCC TCA CGT CCC CGG CAG ACT CCT Ala Phe Gln Ala Gly Ser Phe Leu Ala Ser Arg Pro Arg Gln Thr Pro 525 530 535	1936
TTT GCC GAG AAA TTG GCC AGG ACT CAG GCT GTG GAG TAC TTT GGG GAA Phe Ala Glu Lys Leu Ala Arg Thr Gln Ala Val Glu Tyr Phe Gly Glu 540 545 550	1984
TGG ATC CTT AAC CCC ACC AAC TAT GCC TTT CAG CGA ATT CAC AAC AAT Trp Ile Leu Asn Pro Thr Asn Tyr Ala Phe Gln Arg Ile His Asn Asn 555 560 565	2032
ATG TTT GAT CCA GCC CTG ATT GGT GAC AAG CCA AAG TGG TAT GCT CAT Met Phe Asp Pro Ala Leu Ile Gly Asp Lys Pro Lys Trp Tyr Ala His 570 575 580 585	2080
CAG CTG CAG CCT ATC CAC TAT CGC GTC TAT GAC AGC AAT TCC CAG CTG Gln Leu Gln Pro Ile His Tyr Arg Val Tyr Asp Ser Asn Ser Gln Leu 590 595 600	2128
GCT GAG GCC CTG AGT GTA CCA CCA GAG CGG GAC TCT GAC TCC GAA CCT Ala Glu Ala Leu Ser Val Pro Pro Glu Arg Asp Ser Asp Ser Glu Pro 605 610 615	2176
ACT GAT GAT AGT GGC AGT GAT AGT ATG GAT TAT GAC GAT TCA AGC TCT Thr Asp Asp Ser Gly Ser Asp Ser Met Asp Tyr Asp Ser Ser Ser 620 625 630	2224
TCT TAC TCC TCC CTT GGT GAC TTT GTC AGT GAA ATG ATG AAA TGT GAC Ser Tyr Ser Ser Leu Gly Asp Phe Val Ser Glu Met Met Lys Cys Asp 635 640 645	2272
ATT AAT GGT GAT ACT CCC AAT GTG GAC CCT CTG ACA CAT GCA GCA CTG Ile Asn Gly Asp Thr Pro Asn Val Asp Pro Leu Thr His Ala Ala Leu 650 655 660 665	2320
GGG GAT GCC AGC GAG GTG GAG ATT GAC GAG CTG CAG AAT CAG AAG GAA Gly Asp Ala Ser Glu Val Glu Ile Asp Glu Leu Gln Asn Gln Lys Glu 670 675 680	2368
GCA GAA GAG CCT GGC CCA GAC AGT GAG AAC TCT CAG GAA AAC CCC CCA Ala Glu Glu Pro Gly Pro Asp Ser Glu Asn Ser Gln Glu Asn Pro Pro 685 690 695	2416

CTG Leu	CGC Arg	TCC Ser 700	AGC Ser	TCT Ser	AGC Ser	ACC Thr	ACA Thr 705	GCC Ala	AGC Ser	AGC Ser	AGC Ser	CCC Pro 710	AGC Ser	ACT Thr	GTC Val	2464
ATC Ile	CAC His 715	GGA Gly	GCC Ala	AAC Asn	TCT Ser	GAA Glu 720	CCT Pro	GCT Ala	GAC Asp	TCT Ser	ACG Thr 725	GAG Glu	ATG Met	GAT Asp	GAT Asp	2512
AAG Lys 730	GCA Ala	GCA Ala	GTA Val	GGC Gly 735	GTC Val	TCC Ser	AAG Lys	CCC Pro	CTC Leu	CCT Pro 740	TCC Ser	GTG Val	CCT Pro	CCC Pro	AGC Ser 745	2560
ATT Ile	GGC Gly	AAA Lys	TCG Ser	AAC Asn 750	ATG Met	GAC Asp	AGA Arg	CGT Arg	CAG Gln 755	GCA Ala	GAA Glu	ATT Ile	GGA Gly	GAG Glu 760	GGG Gly	2608
TCA Ser	GTG Val	CGC Arg	CGG Arg 765	CGA Arg	ATC Ile	TAT Tyr	GAC Asp 770	AAT Asn	CCA Pro	TAC Tyr	TTC Phe	GAG Glu	CCC Pro 775	CAA Gln	TAT Tyr	2656
GGC Gly	TTT Phe	CCC Pro 780	CCT Pro	GAG Glu	GAA Glu	GAT Asp	GAG Glu 785	GAT Asp	GAG Glu	CAG Gln	GGG Gly	GAA Glu 790	AGT Ser	TAC Tyr	ACT Thr	2704
CCC Pro	CGA Arg 795	TTC Phe	AGC Ser	CAA Gln	CAT His	GTC Val 800	AGT Ser	GGC Gly	AAT Asn	CGG Arg	GCT Ala 805	CAA Gln	AAG Lys	CTG Leu	CTG Leu	2752
CGG Arg 810	CCC Pro	AAC Asn	AGC Ser	TTG Leu	AGA Arg 815	CTG Leu	GCA Ala	AGT Ser	GAC Asp	TCA Ser 820	GAT Asp	GCA Ala	GAG Glu	TCA Ser	GAC Asp 825	2800
TCT Ser	CGG Arg	GCA Ala	AGC Ser	TCT Ser 830	CCC Pro	AAC Asn	TCC Ser	ACC Thr	GTC Val 835	TCC Ser	AAC Asn	ACC Thr	AGC Ser	ACC Thr 840	GAG Glu	2848
GGC Gly	TTC Phe	GGG Gly 845	GGC Gly	ATC Ile	ATG Met	TCT Ser	TTT Phe 850	GCC Ala	AGC Ser	AGC Ser	CTC Leu	TAT Tyr	CGG Arg 855	AAC Asn	CAC His	2896
AGT Ser	ACC Thr	AGC Ser 860	TTC Phe	AGT Ser	CTT Leu	TCA Ser	AAC Asn 865	CTC Leu	ACA Thr	CTG Leu	CCC Pro	ACC Thr 870	AAA Lys	GGT Gly	GCC Ala	2944
CGA Arg	GAG Glu 875	AAG Lys	GCC Ala	ACG Thr	CCC Pro	TTC Phe 880	CCC Pro	AGT Ser	CTG Leu	AAA Lys	GGA Gly 885	AAC Asn	AGG Arg	AGG Arg	GCG Ala	2992
TTA Leu 890	GTG Val	GAT Asp	CAG Gln	AAG Lys	TCA Ser 895	TCT Ser	GTC Val	ATT Ile	AAA Lys 900	CAC His	AGC Ser	CCA Pro	ACA Thr	GTG Val	AAA Lys 905	3040
AGA Arg	GAA Glu	CCT Pro	CCA Pro	TCA Ser 910	CCC Pro	CAG Gln	GGT Gly	CGA Arg	TCC Ser 915	AGC Ser	AAT Asn	TCT Ser	AGT Ser	GAG Glu 920	AAC Asn	3088
CAG Gln	CAG Gln	TTC Phe 925	CTG Leu	AAG Lys	GAG Glu	GTG Val	GTG Val 930	CAC His	AGC Ser	GTG Val	CTG Leu	GAC Asp	GGC Gly 935	CAG Gln	GGA Gly	3136
GTT Val	GGC Gly	TGG Trp 940	CTC Trp	AAC Asn	ATG Met	AAA Lys	AAG Lys 945	GTG Val	CGC Arg	CGG Arg	CTG Leu	CTG Leu 950	GAG Glu	AGC Ser	GAG Glu	3184
CAG Gln	CTG Leu 955	CGA Arg	GTC Val	TTT Phe	GTC Val 960	CTG Leu	AGC Ser 965	AAG Lys	CTG Leu	AAC Asn	CGC Gly 965	ATG Met	GTG Val	CAG Gln	TCA Ser	3232

GAG Glu 970	GAC Asp	GAT Asp	GCC Ala	CGG Arg	CAG Gln 975	GAC Asp	ATC Ile	ATC Ile	CCG Pro	GAT Asp 980	GTG Val	GAG Glu	ATC Ile	AGT Ser	CGG Arg 985	3280
AAG Lys	GTG Val	TAC Tyr	AAG Lys	GGA Gly 990	ATG Met	TTA Leu	GAC Asp	CTC Leu	CTC Leu 995	AAG Lys	TGT Cys	ACA Thr	GTC Val	CTC Leu 1000	AGC Ser	3328
TTG Leu	GAG Glu	CAG Gln	TCC Ser 1005	TAT Tyr	GCC Ala	CAC His	GCG Ala	GGT Gly 1010	CTG Leu	GGT Gly	GGC Gly	ATG Met	GCC Ala 1015	AGC Ser	ATC Ile	3376
TTT Phe	GGG Gly 1020	CTT Leu	TTG Leu	GAG Glu	ATT Ile	GCC Ala	CAG Gln 1025	ACC Thr	CAC His	TAC Tyr	TAT Tyr	AGT Ser 1030	AAA Lys	GAA Glu	CCA Pro	3424
GAC Asp	AAG Lys 1035	CGG Arg	AAG Lys	AGA Arg	AGT Ser	CCA Pro 1040	ACA Thr	GAA Glu	AGT Ser	GTA Val	AAT Asn 1045	ACC Thr	CCA Pro	GTT Val	GGC Gly	3472
AAG Lys 1050	GAT Asp	CCT Pro	GGC Gly	CTA Leu	GCT Ala 1055	GGG Gly	CGG Arg	GGG Gly	GAC Asp	CCA Pro 1060	AAG Lys	GCT Ala	ATG Met	GCA Ala	CAA Gln 1065	3520
CTG Leu	AGA Arg	GTT Val	CCA Pro	CAA Gln 1070	CTG Leu	GGA Gly	CCT Pro	CGG Arg	GCA Ala 1075	CCA Pro	AGT Ser	GCC Ala	ACA Thr	GGA Gly 1080	AAG Lys	3568
GGT Gly	CCT Pro	AAG Lys 1085	GAA Glu	CTG Leu	GAC Asp	ACC Thr	AGA Arg	AGT Ser 1090	TTA Leu	AAG Lys	GAA Glu	GAA Glu	AAT Asn 1095	TTT Phe	ATA Ile	3616
GCA Ala	TCT Ser 1100	ATT Ile	GGG Gly	CCT Pro	GAA Glu	GTA Val 1105	ATC Ile	AAA Lys	CCT Pro	GTC Val	TTT Phe 1110	GAC Asp	CTT Leu	GGT Gly	GAG Glu	3664
ACA Thr	GAG Glu 1115	GAG Glu	AAA Lys	AAG Lys	TCC Ser	CAG Gln 1120	ATC Ile	AGC Ser	GCA Ala	GAC Asp	AGT Ser 1125	GGT Gly	GTG Val	AGC Ser	CTG Leu	3712
ACG Thr 1130	TCT Ser	AGT Ser	TCC Ser	CAG Gln	AGG Arg 1135	ACT Thr	GAT Asp	CAA Gln	GAC Asp	TCT Ser 1140	GTC Val	ATC Ile	GGC Gly	GTG Val	AGT Ser 1145	3760
CCA Pro	GCT Ala	GTT Val	ATG Met	ATC Ile 1150	CGC Arg	AGC Ser	TCA Ser	AGT Ser	CAG Gln 1155	GAT Asp	TCT Ser	GAA Glu	GTT Val	AGC Ser 1160	ACC Thr	3808
GTG Val	GTG Val	AGT Ser 1165	AAT Asn	AGC Ser	TCT Ser	GGA Gly	GAG Glu	ACC Thr 1170	CTT Leu	GGA Gly	GCT Ala	GAC Asp	AGT Ser 1175	GAC Asp	TTG Leu	3856
AGC Ser	AGC Ser 1180	AAT Asn	GCA Ala	GGT Gly	GAT Asp	GGA Gly	CCA Pro 1185	GGT Gly	GGC Gly	GAG Glu	GGC Gly	AGT Ser 1190	GTT Val	CAC His	CTG Leu	3904
GCA Ala	AGC Ser 1195	TCT Ser	CGG Arg	GGC Gly	ACT Thr	TTG Leu 1200	TCT Ser	GAT Asp	AGT Ser	GAA Glu 1205	ATT Ile	GAG Glu	ACC Thr	AAC Asn	TCT Ser	3952
GCC Ala 1210	ACA Thr	AGC Ser	ACC Thr	ATC Ile	TTT Phe 1215	GGT Gly	AAA Lys	GCC Ala	CAC His	AGC Ser 1220	TTG Leu	AAG Lys	CCA Pro	AGC Ser	ATA Ile 1225	4000
AAG Lys	GAG Glu	AAG Lys	CTG Leu 1230	GCA Ala	GGC Gly	AGC Ser	CCC Pro	ATT Ile	CGT Arg 1235	ACT Thr	TCT Ser	GAA Glu	GAT Asp	GTG Val 1240	AGC Ser	4048

CAG CGA GTC TAT CTC TAT GAG GGA CTC CTA GGC AAA GAG CGT TCT ACT Gln Arg Val Tyr Leu Tyr Glu Gly Leu Leu Gly Lys Glu Arg Ser Thr 1245 1250 1255	4096
TTA TGG GAC CAA ATG CAA TTC TGG GAA GAT GCC TTC TTA GAT GCT GTG Leu Trp Asp Gln Met Gln Phe Trp Glu Asp Ala Phe Leu Asp Ala Val 1260 1265 1270	4144
ATG TTG GAG AGA GAA GGG ATG GGT ATG GAC CAG GGT CCC CAG GAA ATG Met Leu Glu Arg Glu Gly Met Gly Met Asp Gln Gly Pro Gln Glu Met 1275 1280 1285	4192
ATC GAC AGG TAC CTG TCC CTT GGA GAA CAT GAC CGG AAG CGC CTG GAA Ile Asp Arg Tyr Leu Ser Leu Gly Glu His Asp Arg Lys Arg Leu Glu 1290 1295 1300 1305	4240
GAT GAT GAA GAT CGC TTG CTG GCC ACA CTT CTG CAC AAC CTC ATC TCC Asp Asp Glu Asp Arg Leu Leu Ala Thr Leu Leu His Asn Leu Ile Ser 1310 1315 1320	4288
TAC ATG CTG CTG ATG AAG GTA AAT AAG AAT GAC ATC CGC AAG AAG GTG Tyr Met Leu Leu Met Lys Val Asn Lys Asn Asp Ile Arg Lys Lys Val 1325 1330 1335	4336
AGG CGC CTA ATG GGA AAG TCG CAC ATT GGG CTT GTG TAC AGC CAG CAA Arg Arg Leu Met Gly Lys Ser His Ile Gly Leu Val Tyr Ser Gln Gln 1340 1345 1350	4384
ATC AAT GAG GTG CTT GAT CAG CTG GCG AAC CTG AAT GGA CGC GAT CTG Ile Asn Glu Val Leu Asp Gln Leu Ala Asn Leu Asn Gly Arg Asp Leu 1355 1360 1365	4432
TCT ATC TGG TCC AGT GGC AGC CGG CAC ATG AAG AAG CAG ACA TTT GTG Ser Ile Trp Ser Ser Gly Ser Arg His Met Lys Lys Gln Thr Phe Val 1370 1375 1380 1385	4480
GTA CAT GCA GGG ACA GAT ACA AAC GGA GAT ATC TTT TTC ATG GAG GTG Val His Ala Gly Thr Asp Thr Asn Gly Asp Ile Phe Phe Met Glu Val 1390 1395 1400	4528
TGC GAT GAC TGT GTG GTG TTG CGT AGT AAC ATC GGA ACA GTG TAT GAG Cys Asp Asp Cys Val Val Leu Arg Ser Asn Ile Gly Thr Val Tyr Glu 1405 1410 1415	4576
CGC TGG TGG TAC GAG AAG CTC ATC AAC ATG ACC TAC TGT CCC AAG ACG Arg Trp Trp Tyr Glu Lys Leu Ile Asn Met Thr Tyr Cys Pro Lys Thr 1420 1425 1430	4624
AAG GTG TTG TGC TTG TGG CGT AGA AAT GGC TCT GAG ACC CAG CTC AAC Lys Val Leu Cys Leu Trp Arg Arg Asn Gly Ser Glu Thr Gln Leu Asn 1435 1440 1445	4672
AAG TTC TAT ACT AAA AAG TGT CGG GAG CTG TAC TAC TGT GTG AAG GAC Lys Phe Tyr Thr Lys Lys Cys Arg Glu Leu Tyr Tyr Cys Val Lys Asp 1450 1455 1460 1465	4720
AGC ATG GAG CGC GCT GCC GCC CGA CAG CAA AGC ATC AAA CCC GGA CCT Ser Met Glu Arg Ala Ala Ala Arg Gln Gln Ser Ile Lys Pro Gly Pro 1470 1475 1480	4768
GAA TTG GGT GGC GAG TTC CCT GTG CAG GAC CTG AAG ACT GGT GAG GGT Glu Leu Gly Gly Glu Phe Pro Val Gln Asp Leu Lys Thr Gly Glu Gly 1485 1490 1495	4816
GGC CTG CTG CAG GTG ACC CTG GAA GGG ATC AAC CTC AAA TTC ATG CAC Gly Leu Leu Gln Val Thr Leu Glu Gly Ile Asn Leu Lys Phe Met His 1500 1505 1510	4864

AAT CAG GTT TTC ATA GAG CTG AAT CAC ATT AAA AAG TGC AAT ACA GTT	4912
Asn Gln Val Phe Ile Glu Leu Asn His Ile Lys Lys Cys Asn Thr Val	
1515 1520 1525	
CGA GGC GTC TTT GTC CTG GAG GAA TTT GTT CCT GAA ATT AAA GAA GTG	4960
Arg Gly Val Phe Val Leu Glu Glu Phe Val Pro Glu Ile Lys Glu Val	
1530 1535 1540 1545	
GTG AGC CAC AAG TAC AAG ACA CCA ATG GCC CAC GAA ATC TGC TAC TCC	5008
Val Ser His Lys Tyr Lys Thr Pro Met Ala His Glu Ile Cys Tyr Ser	
1550 1555 1560	
GTA TTA TGT CTC TTC TCG TAC GTG GCT GCA GTT CAT AGC AGT GAG GAA	5056
Val Leu Cys Leu Phe Ser Tyr Val Ala Ala Val His Ser Ser Glu Glu	
1565 1570 1575	
GAT CTC AGA ACC CCG CCC CGG CCT GTC TCT AGC TGA TGGAGAGGGG	5102
Asp Leu Arg Thr Pro Pro Arg Pro Val Ser Ser *	
1580 1585	
CTACGCAGCT GCCCCAGCCC AGGGCACGCC CCTGGCCCCCT TGCTGTTCCC AAGTGCACGA	5162
TGCTGCTGTG ACTGAGGAGT GGATGATGCT CGTGTGTCTCT CTGCAAGCCC CCTGCTGTGG	5222
CTTGGTTGGT TACCGGTTAT GTGTCCCTCT GAGTGTGTCT TGAGCGTGTC CACCTTCTCC	5282
CTCTCCACTC CCAGAAGACC AAAGTGCCTT CCCCTCAGGG CTCAAGAATG TGTACAGTCT	5342
GTGGGGCCGG TGTGAACCCA CTATTTTGTG TCCTTGAGAC ATTTGTGTTG TGGTTCCTTG	5402
TCCTTGTCCTC TGGCGTTATA ACTGTCCACT GCAAGAGTCT GGCTCTCCCT TCTCTGTGAC	5462
CCGGCATGAC TGGGCGCCTG GAGCAGTTTC ACTCTGTGAG GAGTGAGGGA ACCCTGGGGC	5522
TCACCTCTC AGAGGAAGGG CACAGAGAGG AAGGGAAGAA TTGGGGGGCA GCCCGAGTGA	5582
GTGGCAGCCT CCCTGCTTCC TTCTGCATTC CCAAGCCGGC AGCTACTGCC CAGGGCCCGC	5642
AGTGTGGGCT GCTGCCTGCC ACAGCCTCTG TGAAGTGCAGT GGAGCGGCGA ATTCCCTGTG	5702
GCCTGCCACG CCTTCGGCAT CAGAGGATGG AGTGGTCGAG GCTAGTGGAG TCCCAGGGAC	5762
CGCTGGCTGC TCTGCCTGAG CATCAGGGAG GGGGCAAGAA AGACCAAGCT GGGTTTGCAC	5822
ATCTGTCTGC AGGCTGTCTC TCCAGGCACG GGGTGTGAGG AGGGAGAGAC AGCCTGGGTA	5882
TGGGCAAGAA ATGACTGTAA ATATTTTCAGC CCCACATTAT TTATAGAAAA TGTACAGTTG	5942
TGTGAATGTG AAATAAATGT CCTCAACTCC CAAAAAAAAA AAAAAAAAAA AAAAAAAAAA	6002

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1589 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Met Val Gln Lys Lys Lys Phe Cys Pro Arg Leu Leu Asp Tyr Leu Val
1 5 10 15

Ile Val Gly Ala Arg His Pro Ser Ser Asp Ser Val Ala Gln Thr Pro

20							25							30						
Glu	Leu	Leu	Arg	Arg	Tyr	Pro	Leu	Glu	Asp	His	Thr	Glu	Phe	Pro	Leu					
		35					40					45								
Pro	Pro	Asp	Val	Val	Phe	Phe	Cys	Gln	Pro	Glu	Gly	Cys	Leu	Ser	Val					
	50					55					60									
Arg	Gln	Arg	Arg	Met	Ser	Leu	Arg	Asp	Asp	Thr	Ser	Phe	Val	Phe	Thr					
65					70					75					80					
Leu	Thr	Asp	Lys	Asp	Thr	Gly	Val	Thr	Arg	Tyr	Gly	Ile	Cys	Val	Asn					
				85					90					95						
Phe	Tyr	Arg	Ser	Phe	Gln	Lys	Arg	Ile	Ser	Lys	Glu	Lys	Gly	Glu	Gly					
			100					105					110							
Gly	Ala	Gly	Ser	Arg	Gly	Lys	Glu	Gly	Thr	His	Ala	Thr	Cys	Ala	Ser					
		115					120					125								
Glu	Glu	Gly	Gly	Thr	Glu	Ser	Ser	Glu	Ser	Gly	Ser	Ser	Leu	Gln	Pro					
	130					135					140									
Leu	Ser	Ala	Asp	Ser	Thr	Pro	Asp	Val	Asn	Gln	Ser	Pro	Arg	Gly	Lys					
145					150					155					160					
Arg	Arg	Ala	Lys	Ala	Gly	Ser	Arg	Ser	Arg	Asn	Ser	Thr	Leu	Thr	Ser					
				165					170					175						
Leu	Cys	Val	Leu	Ser	His	Tyr	Pro	Phe	Phe	Ser	Thr	Phe	Arg	Glu	Cys					
			180					185					190							
Leu	Tyr	Thr	Leu	Lys	Arg	Leu	Val	Asp	Cys	Cys	Ser	Glu	Arg	Leu	Leu					
	195					200						205								
Gly	Lys	Lys	Leu	Gly	Ile	Pro	Arg	Gly	Val	Gln	Arg	Asp	Thr	Met	Trp					
	210					215					220									
Arg	Ile	Phe	Thr	Gly	Ser	Leu	Leu	Val	Glu	Glu	Lys	Ser	Ser	Ala	Leu					
225				230						235					240					
Leu	His	Asp	Leu	Arg	Glu	Ile	Glu	Ala	Trp	Ile	Tyr	Arg	Leu	Leu	Arg					
				245					250					255						
Ser	Pro	Val	Pro	Val	Ser	Gly	Gln	Lys	Arg	Val	Asp	Ile	Glu	Val	Leu					
			260					265					270							
Pro	Gln	Glu	Leu	Gln	Pro	Ala	Leu	Thr	Phe	Ala	Leu	Pro	Asp	Pro	Ser					
		275					280					285								
Arg	Phe	Thr	Leu	Val	Asp	Phe	Pro	Leu	His	Leu	Pro	Leu	Glu	Leu	Leu					
	290					295					300									
Gly	Val	Asp	Ala	Cys	Leu	Gln	Val	Leu	Thr	Cys	Ile	Leu	Leu	Glu	His					
305					310					315					320					
Lys	Val	Val	Leu	Gln	Ser	Arg	Asp	Tyr	Asn	Ala	Leu	Ser	Met	Ser	Val					
				325					330					335						
Met	Ala	Phe	Val	Ala	Met	Ile	Tyr	Pro	Leu	Glu	Tyr	Met	Phe	Pro	Val					
			340					345					350							
Ile	Pro	Leu	Leu	Pro	Thr	Cys	Met	Ala	Ser	Ala	Glu	Gln	Leu	Leu	Leu					
		355					360					365								
Ala	Pro	Thr	Pro																	

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Lys Leu Asp Phe Lys Met Pro Asp Asp Val Trp Leu Val Asp Leu Asp
 385 390 395 400
 Ser Asn Arg Val Ile Ala Pro Thr Asn Ala Glu Val Leu Pro Ile Leu
 405 410 415
 Pro Glu Pro Glu Ser Leu Glu Leu Lys Lys His Leu Lys Gln Ala Leu
 420 425 430
 Ala Ser Met Ser Leu Asn Thr Gln Pro Ile Leu Asn Leu Glu Lys Phe
 435 440 445
 His Glu Gly Gln Glu Ile Pro Leu Leu Leu Gly Arg Pro Ser Asn Asp
 450 455 460
 Leu Gln Ser Thr Pro Ser Thr Glu Phe Asn Pro Leu Ile Tyr Gly Asn
 465 470 475 480
 Asp Val Asp Ser Val Asp Val Ala Thr Arg Val Ala Met Val Arg Phe
 485 490 495
 Phe Asn Ser Ala Asn Val Leu Gln Gly Phe Gln Met His Thr Arg Thr
 500 505 510
 Leu Arg Leu Phe Pro Arg Pro Val Val Ala Phe Gln Ala Gly Ser Phe
 515 520 525
 Leu Ala Ser Arg Pro Arg Gln Thr Pro Phe Ala Glu Lys Leu Ala Arg
 530 535 540
 Thr Gln Ala Val Glu Tyr Phe Gly Glu Trp Ile Leu Asn Pro Thr Asn
 545 550 555 560
 Tyr Ala Phe Gln Arg Ile His Asn Asn Met Phe Asp Pro Ala Leu Ile
 565 570 575
 Gly Asp Lys Pro Lys Trp Tyr Ala His Gln Leu Gln Pro Ile His Tyr
 580 585 590
 Arg Val Tyr Asp Ser Asn Ser Gln Leu Ala Glu Ala Leu Ser Val Pro
 595 600 605
 Pro Glu Arg Asp Ser Asp Ser Glu Pro Thr Asp Asp Ser Gly Ser Asp
 610 615 620
 Ser Met Asp Tyr Asp Asp Ser Ser Ser Ser Tyr Ser Ser Leu Gly Asp
 625 630 635 640
 Phe Val Ser Glu Met Met Lys Cys Asp Ile Asn Gly Asp Thr Pro Asn
 645 650 655
 Val Asp Pro Leu Thr His Ala Ala Leu Gly Asp Ala Ser Glu Val Glu
 660 665 670
 Ile Asp Glu Leu Gln Asn Gln Lys Glu Ala Glu Glu Pro Gly Pro Asp
 675 680 685
 Ser Glu Asn Ser Gln Glu Asn Pro Pro Leu Arg Ser Ser Ser Ser Thr
 690 695 700
 Thr Ala Ser Ser Ser Pro Ser Thr Val Ile His Gly Ala Asn Ser Glu
 705 710 715 720
 Pro Ala Asp Ser Thr Glu Met Asp Asp Lys Ala Ala Val Gly Val Ser
 725 730 735
 Lys Pro Leu Pro Ser Val Pro Pro Ser Ile Gly Lys Ser Asn Met Asp

740										745					750				
Arg	Arg	Gln	Ala	Glu	Ile	Gly	Glu	Gly	Ser	Val	Arg	Arg	Arg	Ile	Tyr				
		755					760					765							
Asp	Asn	Pro	Tyr	Phe	Glu	Pro	Gln	Tyr	Gly	Phe	Pro	Pro	Glu	Glu	Asp				
		770				775					780								
Glu	Asp	Glu	Gln	Gly	Glu	Ser	Tyr	Thr	Pro	Arg	Phe	Ser	Gln	His	Val				
785					790					795					800				
Ser	Gly	Asn	Arg	Ala	Gln	Lys	Leu	Leu	Arg	Pro	Asn	Ser	Leu	Arg	Leu				
				805					810					815					
Ala	Ser	Asp	Ser	Asp	Ala	Glu	Ser	Asp	Ser	Arg	Ala	Ser	Ser	Pro	Asn				
			820					825					830						
Ser	Thr	Val	Ser	Asn	Thr	Ser	Thr	Glu	Gly	Phe	Gly	Gly	Ile	Met	Ser				
		835					840					845							
Phe	Ala	Ser	Ser	Leu	Tyr	Arg	Asn	His	Ser	Thr	Ser	Phe	Ser	Leu	Ser				
	850					855					860								
Asn	Leu	Thr	Leu	Pro	Thr	Lys	Gly	Ala	Arg	Glu	Lys	Ala	Thr	Pro	Phe				
865					870					875					880				
Pro	Ser	Leu	Lys	Gly	Asn	Arg	Arg	Ala	Leu	Val	Asp	Gln	Lys	Ser	Ser				
				885					890					895					
Val	Ile	Lys	His	Ser	Pro	Thr	Val	Lys	Arg	Glu	Pro	Pro	Ser	Pro	Gln				
			900					905					910						
Gly	Arg	Ser	Ser	Asn	Ser	Ser	Glu	Asn	Gln	Gln	Phe	Leu	Lys	Glu	Val				
		915					920					925							
Val	His	Ser	Val	Leu	Asp	Gly	Gln	Gly	Val	Gly	Trp	Leu	Asn	Met	Lys				
	930					935					940								
Lys	Val	Arg	Arg	Leu	Leu	Glu	Ser	Glu	Gln	Leu	Arg	Val	Phe	Val	Leu				
945					950					955					960				
Ser	Lys	Leu	Asn	Arg	Met	Val	Gln	Ser	Glu	Asp	Asp	Ala	Arg	Gln	Asp				
				965					970					975					
Ile	Ile	Pro	Asp	Val	Glu	Ile	Ser	Arg	Lys	Val	Tyr	Lys	Gly	Met	Leu				
			980					985					990						
Asp	Leu	Leu	Lys	Cys	Thr	Val	Leu	Ser	Leu	Glu	Gln	Ser	Tyr	Ala	His				
		995					1000					1005							
Ala	Gly	Leu	Gly	Gly	Met	Ala	Ser	Ile	Phe	Gly	Leu	Leu	Glu	Ile	Ala				
	1010					1015					1020								
Gln	Thr	His	Tyr	Tyr	Ser	Lys	Glu	Pro	Asp	Lys	Arg	Lys	Arg	Ser	Pro				
1025					1030					1035					1040				
Thr	Glu	Ser	Val	Asn	Thr	Pro	Val	Gly	Lys	Asp	Pro	Gly	Leu	Ala	Gly				
				1045					1050					1055					
Arg	Gly	Asp	Pro	Lys	Ala	Met	Ala	Gln	Leu	Arg	Val	Pro	Gln	Leu	Gly				
			1060					1065					1070						
Pro	Arg	Ala	Pro	Ser	Ala	Thr	Gly	Lys	Gly	Pro	Lys	Glu	Leu	Asp	Thr				
		1075					1080					1085							

Ile	Lys	Pro	Val	Phe	Asp	Leu	Gly	Glu	Thr	Glu	Glu	Lys	Lys	Ser	Gln	1105	1110	1115	1120
Ile	Ser	Ala	Asp	Ser	Gly	Val	Ser	Leu	Thr	Ser	Ser	Ser	Gln	Arg	Thr	1125	1130	1135	
Asp	Gln	Asp	Ser	Val	Ile	Gly	Val	Ser	Pro	Ala	Val	Met	Ile	Arg	Ser	1140	1145	1150	
Ser	Ser	Gln	Asp	Ser	Glu	Val	Ser	Thr	Val	Val	Ser	Asn	Ser	Ser	Gly	1155	1160	1165	
Glu	Thr	Leu	Gly	Ala	Asp	Ser	Asp	Leu	Ser	Ser	Asn	Ala	Gly	Asp	Gly	1170	1175	1180	
Pro	Gly	Gly	Glu	Gly	Ser	Val	His	Leu	Ala	Ser	Ser	Arg	Gly	Thr	Leu	1185	1190	1195	1200
Ser	Asp	Ser	Glu	Ile	Glu	Thr	Asn	Ser	Ala	Thr	Ser	Thr	Ile	Phe	Gly	1205	1210	1215	
Lys	Ala	His	Ser	Leu	Lys	Pro	Ser	Ile	Lys	Glu	Lys	Leu	Ala	Gly	Ser	1220	1225	1230	
Pro	Ile	Arg	Thr	Ser	Glu	Asp	Val	Ser	Gln	Arg	Val	Tyr	Leu	Tyr	Glu	1235	1240	1245	
Gly	Leu	Leu	Gly	Lys	Glu	Arg	Ser	Thr	Leu	Trp	Asp	Gln	Met	Gln	Phe	1250	1255	1260	
Trp	Glu	Asp	Ala	Phe	Leu	Asp	Ala	Val	Met	Leu	Glu	Arg	Glu	Gly	Met	1265	1270	1275	1280
Gly	Met	Asp	Gln	Gly	Pro	Gln	Glu	Met	Ile	Asp	Arg	Tyr	Leu	Ser	Leu	1285	1290	1295	
Gly	Glu	His	Asp	Arg	Lys	Arg	Leu	Glu	Asp	Asp	Glu	Asp	Arg	Leu	Leu	1300	1305	1310	
Ala	Thr	Leu	Leu	His	Asn	Leu	Ile	Ser	Tyr	Met	Leu	Leu	Met	Lys	Val	1315	1320	1325	
Asn	Lys	Asn	Asp	Ile	Arg	Lys	Lys	Val	Arg	Arg	Leu	Met	Gly	Lys	Ser	1330	1335	1340	
His	Ile	Gly	Leu	Val	Tyr	Ser	Gln	Gln	Ile	Asn	Glu	Val	Leu	Asp	Gln	1345	1350	1355	1360
Leu	Ala	Asn	Leu	Asn	Gly	Arg	Asp	Leu	Ser	Ile	Trp	Ser	Ser	Gly	Ser	1365	1370	1375	
Arg	His	Met	Lys	Lys	Gln	Thr	Phe	Val	Val	His	Ala	Gly	Thr	Asp	Thr	1380	1385	1390	
Asn	Gly	Asp	Ile	Phe	Phe	Met	Glu	Val	Cys	Asp	Asp	Cys	Val	Val	Leu	1395	1400	1405	
Arg	Ser	Asn	Ile	Gly	Thr	Val	Tyr	Glu	Arg	Trp	Trp	Tyr	Glu	Lys	Leu	1410	1415	1420	
Ile	Asn	Met	Thr	Tyr	Cys	Pro	Lys	Thr	Lys	Val	Leu	Cys	Leu	Trp	Arg	1425	1430	1435	1440
Arg	Asn	Gly	Ser	Glu	Thr	Gln	Leu	Asn	Lys	Phe	Tyr	Thr	Lys	Lys	Cys	1445	1450	1455	
Arg	Glu	Leu	Tyr	Tyr	Cys	Val	Lys	Asp	Ser	Met	Glu	Arg	Ala	Ala	Ala				

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1460	1465	1470
Arg Gln Gln Ser Ile Lys Pro Gly Pro Glu Leu Gly Gly Glu Phe Pro		
1475	1480	1485
Val Gln Asp Leu Lys Thr Gly Glu Gly Gly Leu Leu Gln Val Thr Leu		
1490	1495	1500
Glu Gly Ile Asn Leu Lys Phe Met His Asn Gln Val Phe Ile Glu Leu -		
1505	1510	1515 1520
Asn His Ile Lys Lys Cys Asn Thr Val Arg Gly Val Phe Val Leu Glu		
1525	1530	1535
Glu Phe Val Pro Glu Ile Lys Glu Val Val Ser His Lys Tyr Lys Thr		
1540	1545	1550
Pro Met Ala His Glu Ile Cys Tyr Ser Val Leu Cys Leu Phe Ser Tyr		
1555	1560	1565
Val Ala Ala Val His Ser Ser Glu Glu Asp Leu Arg Thr Pro Pro Arg		
1570	1575	1580
Pro Val Ser Ser *		
1585		

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2473 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
- (A) NAME/KEY: CDS
 - (B) LOCATION: 14..2404

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

CCGACGAGGA GACATGGCGG CGGCGCCGGT AGCGGCTGGG TCTGGAGCCG GCCGAGGGAG	60
ACGGTCGGCA GCCACAGTGG CGGCTTGGGG CGGATGGGGC GGCCGGCCGC GGCCTGGTAA	120
CATTCTGCTG CAGCTGCGGC AGGGCCAGCT GACCGGCCGG GGCCTGGTCC GGGCGGTGCA	180
GTTCACTGAG ACTTTTTTGA CGGAGAGGGA CAAACAATCC AAGTGGAGTG GAATTCCTCA	240
GCTGCTCCTC AAGCTGCACA CCACCAGCCA CCTCCACAGT GACTTTGTTG AGTGTCAAAA	300
CATCCTCAAG GAAATTTCTC CTCTTCTCTC CATGGAGGCT ATGGCATTTC TTAAGAAGA	360
GAGGAAACTT ACCCAAGAAA CCACTTATCC AAATACTTAC ATTTTGGACT TGTTTGGAGG	420
TGTTGATCTT CTTGTAGAAA TTCTTATGAG GCCTACGATC TCTATCCGGG GACAGAACT	480
GAAAATAAGT GATGAAATGT CCAAGGACTG CTTGAGTATC CTGTATAATA CCTGTGTCTG	540
TACAGAGGGA GTTACAAAGC GTTGGCAGA AAAGAATGAC TTTGTGATCT TCCTGTTTAC	600
ATTGATGACA AGTAAGAAGA CATTCTTACA AACAGCAACC CTCATTGAAG ATATTTTAGG	660

TGTTAAAAAG	GAAATGATCC	GACTAGATGA	AGTCCCCAAT	CTGAGTTCCT	TAGTATCCAA	720
TTTCGATCAG	CAGCAGCTCG	CTAATTTCTG	CCGGATTCTG	GCTGTCAACA	TTTCAGAGAT	780
GGATACAGGG	AATGATGACA	AGCACACGCT	TCTTGCCAAA	AATGCTCAAC	AGAAGAAGAG	840
CTTGAGTTTG	GGGCCTTCTG	CAGCTGAAAT	CAATCAAGCG	GCCCTTCTCA	GCATTCCTGG	900
CTTTGTTGAG	CGGCTTTGCA	AACTGGCGAC	TCGAAAGGTG	TCAGAGTCAA	CGGGCACAGE	960
CAGCTTCCTT	CAGGAGTTGG	AAGAGTGGTA	CACATGGCTA	GACAATGCTT	TGGTGCTAGA	1020
TGCCCTGATG	CGAGTGGCCA	ATGAGGAGTC	AGAGCACAAT	CAAGCCTCCA	TTGTGTTCCC	1080
TCCTCCAGGG	GCTTCTGAGG	AGAATGGCCT	GCCTCACACG	TCAGCCAGAA	CCCAGCTGCC	1140
CCAGTCAATG	AAGATTATGC	ATGAGATCAT	GTACAAACTG	GAAGTGCTCT	ATGTCCTCTG	1200
CGTGCTGCTG	ATGGGGCGTC	AGCGAAACCA	GGTTCACAGA	ATGATTGCAG	AGTTCAAGCT	1260
GATCCCTGGA	CTTAATAATT	TGTTTGACAA	ACTGATTTGG	AGGAAGCATT	CAGCATCTGC	1320
CCTTGTCCTC	CATGGTCACA	ACCAGAACTG	TGACTGTAGC	CCGGACATCA	CCTTGAAGAT	1380
ACAGTTTTTG	AGGCTTCTTC	AGAGCTTCAG	TGACCACCAC	GAGAACAAGT	ACTTGTTACT	1440
CAACAACCAG	GAGCTGAATG	AACTCAGTGC	CATCTCTCTC	AAGGCCAACA	TCCCTGAGGT	1500
GGAAGCTGTC	CTCAACACCG	ACAGGAGTTT	GGTGTGTGAT	GGGAAGAGGG	GCTTATTAAC	1560
TCGTCTGCTG	CAGGTCATGA	AGAAGGAGCC	AGCAGAGTCG	TCTTTCAGGT	TTTGGCAAGC	1620
TCGGGCTGTG	GAGAGTTTCC	TCCGAGGGAC	CACCTCCTAT	GCAGACCAGA	TGTTCTCTGT	1680
GAAGCGAGGC	CTCTTGAGGC	ACATCCTTTA	CTGCATTGTG	GACAGCGAGT	GTAAGTCAAG	1740
GGATGTGCTC	CAGAGTTACT	TTGACCTCCT	GGGGGAGCTG	ATGAAGTTCA	ACGTTGATGC	1800
ATTCAAGAGA	TTCAATAAAA	ATATCAACAC	CGATGCAAAG	TTCCAGGTAT	TCCTGAAGCA	1860
GATCAACAGC	TCCCTGGTGG	ACTCCAACAT	GCTGGTGCGC	TGTGTCACTC	TGTCCCTGGA	1920
CCGATTTGAA	AACCAGGTGG	ATATGAAAAGT	TGCCGAGGTA	CTGTCTGAAT	GCCGCCTGCT	1980
CGCTACATA	TCCCAGGTGC	CCACGCAGAT	GTCTTCTCTC	TTCCGCCTCA	TCAACATCAT	2040
CCACGTGCAG	ACGCTGACCC	AGGAGAACGT	CAGCTGCCTC	AACACCAGCC	TGGTGATCCT	2100
GATGCTGGCC	CGACGGAAG	AGCGGCTGCC	CCTGTACCTG	CGGCTGCTGC	AGCGGATGGA	2160
GCACAGCAAG	AAGTACCCCG	GCTTCTCTGT	CAACAACCTT	CACAACCTGC	TGCGCTTCTG	2220
GCAGCAGCAC	TACCTGCACA	AGGACAAGGA	CAGCACCTGC	CTAGAGAACA	GCTCCTGCAT	2280
CAGCTTCTCA	TACTGGAAGG	AGACAGTGTC	CATCCTGTTG	AACCCGGACC	GGCAGTCAAC	2340
CTCTGCTCTC	GTTAGCTACA	TTGAGGAGCC	CTACATGGAC	ATAGACAGGG	ACTTCACTGA	2400
GGAGTGACCT	TGGGCCAGGC	CTCGGGAGGC	TGCTGGGCCA	GTGTGGGTGA	GCGTGGGTAC	2460
GATGCCACAC	GCC					2475

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 797 amino acids
(B) TYPE: amino acid

(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Met	Ala	Ala	Ala	Pro	Val	Ala	Ala	Gly	Ser	Gly	Ala	Gly	Arg	Gly	Arg	1	5	10	15
Arg	Ser	Ala	Ala	Thr	Val	Ala	Ala	Trp	Gly	Gly	Trp	Gly	Gly	Arg	Pro	20	25	30	
Arg	Pro	Gly	Asn	Ile	Leu	Leu	Gln	Leu	Arg	Gln	Gly	Gln	Leu	Thr	Gly	35	40	45	
Arg	Gly	Leu	Val	Arg	Ala	Val	Gln	Phe	Thr	Glu	Thr	Phe	Leu	Thr	Glu	50	55	60	
Arg	Asp	Lys	Gln	Ser	Lys	Trp	Ser	Gly	Ile	Pro	Gln	Leu	Leu	Leu	Lys	65	70	75	80
Leu	His	Thr	Thr	Ser	His	Leu	His	Ser	Asp	Phe	Val	Glu	Cys	Gln	Asn	85	90	95	
Ile	Leu	Lys	Glu	Ile	Ser	Pro	Leu	Leu	Ser	Met	Glu	Ala	Met	Ala	Phe	100	105	110	
Val	Thr	Glu	Glu	Arg	Lys	Leu	Thr	Gln	Glu	Thr	Thr	Tyr	Pro	Asn	Thr	115	120	125	
Tyr	Ile	Phe	Asp	Leu	Phe	Gly	Gly	Val	Asp	Leu	Leu	Val	Glu	Ile	Leu	130	135	140	
Met	Arg	Pro	Thr	Ile	Ser	Ile	Arg	Gly	Gln	Lys	Leu	Lys	Ile	Ser	Asp	145	150	155	160
Glu	Met	Ser	Lys	Asp	Cys	Leu	Ser	Ile	Leu	Tyr	Asn	Thr	Cys	Val	Cys	165	170	175	
Thr	Glu	Gly	Val	Thr	Lys	Arg	Leu	Ala	Glu	Lys	Asn	Asp	Phe	Val	Ile	180	185	190	
Phe	Leu	Phe	Thr	Leu	Met	Thr	Ser	Lys	Lys	Thr	Phe	Leu	Gln	Thr	Ala	195	200	205	
Thr	Leu	Ile	Glu	Asp	Ile	Leu	Gly	Val	Lys	Lys	Glu	Met	Ile	Arg	Leu	210	215	220	
Asp	Glu	Val	Pro	Asn	Leu	Ser	Ser	Leu	Val	Ser	Asn	Phe	Asp	Gln	Gln	225	230	235	240
Gln	Leu	Ala	Asn	Phe	Cys	Arg	Ile	Leu	Ala	Val	Thr	Ile	Ser	Glu	Met	245	250	255	
Asp	Thr	Gly	Asn	Asp	Asp	Lys	His	Thr	Leu	Leu	Ala	Lys	Asn	Ala	Gln	260	265	270	
Gln	Lys	Lys	Ser	Leu	Ser	Leu	Gly	Pro	Ser	Ala	Ala	Glu	Ile	Asn	Gln	275	280	285	
Ala	Ala	Leu	Leu	Ser	Ile	Pro	Gly	Phe	Val	Glu	Arg	Leu	Cys	Lys	Leu	290	295	300	

Ala	Thr	Arg	Lys	Val	Ser	Glu	Ser	Thr	Gly	Thr	Ala	Ser	Phe	Leu	Gln	305	310	315	320
Glu	Leu	Glu	Glu	Trp	Tyr	Thr	Trp	Leu	Asp	Asn	Ala	Leu	Val	Leu	Asp	325	330	335	
Ala	Leu	Met	Arg	Val	Ala	Asn	Glu	Glu	Ser	Glu	His	Asn	Gln	Ala	Ser	340	345	350	
Ile	Val	Phe	Pro	Pro	Pro	Gly	Ala	Ser	Glu	Glu	Asn	Gly	Leu	Pro	His	355	360	365	
Thr	Ser	Ala	Arg	Thr	Gln	Leu	Pro	Gln	Ser	Met	Lys	Ile	Met	His	Glu	370	375	380	
Ile	Met	Tyr	Lys	Leu	Glu	Val	Leu	Tyr	Val	Leu	Cys	Val	Leu	Leu	Met	385	390	395	400
Gly	Arg	Gln	Arg	Asn	Gln	Val	His	Arg	Met	Ile	Ala	Glu	Phe	Lys	Leu	405	410	415	
Ile	Pro	Gly	Leu	Asn	Asn	Leu	Phe	Asp	Lys	Leu	Ile	Trp	Arg	Lys	His	420	425	430	
Ser	Ala	Ser	Ala	Leu	Val	Leu	His	Gly	His	Asn	Gln	Asn	Cys	Asp	Cys	435	440	445	
Ser	Pro	Asp	Ile	Thr	Leu	Lys	Ile	Gln	Phe	Leu	Arg	Leu	Leu	Gln	Ser	450	455	460	
Phe	Ser	Asp	His	His	Glu	Asn	Lys	Tyr	Leu	Leu	Leu	Asn	Asn	Gln	Glu	465	470	475	480
Leu	Asn	Glu	Leu	Ser	Ala	Ile	Ser	Leu	Lys	Ala	Asn	Ile	Pro	Glu	Val	485	490	495	
Glu	Ala	Val	Leu	Asn	Thr	Asp	Arg	Ser	Leu	Val	Cys	Asp	Gly	Lys	Arg	500	505	510	
Gly	Leu	Leu	Thr	Arg	Leu	Leu	Gln	Val	Met	Lys	Lys	Glu	Pro	Ala	Glu	515	520	525	
Ser	Ser	Phe	Arg	Phe	Trp	Gln	Ala	Arg	Ala	Val	Glu	Ser	Phe	Leu	Arg	530	535	540	
Gly	Thr	Thr	Ser	Tyr	Ala	Asp	Gln	Met	Phe	Leu	Leu	Lys	Arg	Gly	Leu	545	550	555	560
Leu	Glu	His	Ile	Leu	Tyr	Cys	Ile	Val	Asp	Ser	Glu	Cys	Lys	Ser	Arg	565	570	575	
Asp	Val	Leu	Gln	Ser	Tyr	Phe	Asp	Leu	Leu	Gly	Glu	Leu	Met	Lys	Phe	580	585	590	
Asn	Val	Asp	Ala	Phe	Lys	Arg	Phe	Asn	Lys	Asn	Ile	Asn	Thr	Asp	Ala	595	600	605	
Lys	Phe	Gln	Val	Phe	Leu	Lys	Gln	Ile	Asn	Ser	Ser	Leu	Val	Asp	Ser	610	615	620	
Asn	Met	Leu	Val	Arg	Cys	Val	Thr	Leu	Ser	Leu	Asp	Arg	Phe	Glu	Asn	625	630	635	640
Gln	Val	Asp	Met	Lys	Val	Ala	Glu	Val	Leu	Ser	Glu	Cys	Arg	Leu	Leu	645	650	655	
Ala	Tyr	Ile	Ser	Gln	Val	Pro	Thr	Gln	Met	Ser	Phe	Leu	Phe	Arg	Leu				

